

Run on: March 26, 2003, 19:28:58 ; Search time 75 Seconds

(without alignments)
614.730 Million cell updates/sec

Title: US-09-942-374-2

Sequence: 1 MYNGSCCRIEGDTISQVMP...ANSFQSQSDGQWDPHIVEWH 346

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 300000000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database

1:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT *
2:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT *
3:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT *
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6:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT *
7:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT *
8:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT *
9:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT *
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12:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT *
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19:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT *
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21:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT *
22:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT *
23:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	Length	DB	ID	Description
1	1853	100.0	346	22	ABBA4522		Human GPCR1A polypeptide
2	1853	100.0	346	22	AAU06197		Novel human G protein-coupled receptor
3	1853	100.0	346	22	AAU04373		Human G-protein coupled receptor 1
4	1853	100.0	346	22	AAAG80968		Human nGPR1 #2
5	1853	100.0	346	23	AAE24354		Human G protein coupled receptor 1
6	1853	100.0	346	23	AAO14788		Human G protein coupled receptor 1
7	1853	100.0	346	23	AAE08596		Human lipocyte-orientated G-protein coupled receptor 1
8	1853	100.0	346	23	AAE16172		Human G-protein coupled receptor 1
9	1853	100.0	346	23	AAU11401		HM74-like G-protein coupled receptor
10	1853	100.0	346	23	AAE17077		Human G-protein coupled receptor 1

11	1839	99.2	346	22	ABBA44523	Human GPCR16 polypeptide
12	1570	84.7	296	66	AAAG80930	Human nGPCR11 #1
13	897.5	48.4	387	23	AAU779992	Human Inflammation
14	883.5	47.7	363	20	AAW94654	G-protein coupled
15	883.5	47.7	363	22	AAU04379	Human G-protein co
16	881.5	47.6	387	21	AAAY0672	Human mutant G prc
17	880.5	47.5	387	21	AAAY0637	Human G protein-co
18	880.5	47.5	387	23	AAU79041	Human G protein-co
19	879.5	47.5	363	23	AAU77993	Human Inflammation
20	529	28.5	384	22	AAEB2493	Human Inflammation
21	529	28.5	384	23	AAU74911	Human CN103 G prc
22	529	28.5	423	23	AAW88460	Human 7-transmembr
23	529	28.5	423	22	AAAG78785	Amino acid sequenc
24	529	28.5	423	22	AAU04365	Human 7-transmembr
25	529	28.5	455	21	AAAY94339	Human opioid-type
26	510	27.5	476	20	AAW88461	Human G-protein co
27	451.5	24.4	319	21	AAAY9157	Human cell surface
28	450.5	24.3	319	21	AAAY9157	Human 7-transmembr
29	448.5	24.2	319	23	AAEB6376	Human G-protein co
30	448.5	24.2	319	21	AAAY0625	Human G-protein co
31	448.5	24.2	319	21	AAAY0659	Human G-protein co
32	366.5	19.8	330	23	AAAG77964	Human mutant G prc
33	366.5	19.8	330	23	AAAG77964	Human G-protein co
34	366.5	19.8	346	22	AAAE07539	Human G-protein co
35	366.5	19.8	346	22	AAEL12032	Human G-protein co
36	366.5	19.8	346	22	AAEB2882	Human P2Y-like GPCR
37	366.5	19.8	346	22	AAEB07538	Human G-protein co
38	366.5	19.8	346	22	AAU04368	Human G-protein co
39	366.5	19.8	346	22	AAU04383	Human G-protein co
40	366.5	19.8	346	22	AAU07297	Cysteinyl leukotri-
41	366.5	19.8	346	23	AAAB73097	Human ITCA4 receptor
42	366.5	19.8	346	23	ABG66684	Human novel polypep
43	366.5	19.8	346	23	AAU10004	Human CysLT2-like
44	366.5	19.8	346	23	AAEL17231	Human CysLT2 GPCR
45	366.5	19.8	346	23	AAAG7965	Human G-protein co
46	366.5	19.8	346	23	ABBO57295	Human LTD4-like G

ALIGNMENTS

RESULT 1
ABB44522

AC ABB44522;

DT 28-JAN-2002 (first entry)
 YY

	Human GPCR1a polypeptide	SEQ ID NO 2.
DE		
XX		

KW	human; G-protein-coupled protein-receptor; cardiac; antiarteriosclerotic
KW	anabolic; cytotastic; antiviral; gene therapy; cardiomyopathy; obesity;
KW	anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
KW	asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
KW	infection; human immunodeficiency virus; HIV.
XX	
OS	Homo sapiens.

Homo sapiens.

PN W0200174904-A2

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US10241.
YY

PR 31-MAR-2000; 2000US-1936664P.
PR 05-APR-2000; 2000US-194614P

PR 06-APR-2000; 2000US-195063P.
PR 06-APR-2000; 2000US-195066P

06-APR-2000: 2000MS-195058P
06-APR-2000: 2000US-195067P

06-APR-2000: 2000US-195070P

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PR 21-JUL-2000; 2000US-219855P.
 PR 27-JUL-2000; 2000US-221284P.
 PR 28-JUL-2000; 2000US-221325P.
 PR 11-AUG-2000; 2000US-224588P.
 PR 11-OCT-2000; 2000US-239613P.
 PR 18-JAN-2001; 2001US-262508P.
 PR 23-JAN-2001; 2001US-263433P.
 PR 23-JAN-2001; 2001US-263604P.
 PR 30-JAN-2001; 2001US-265161P.
 PR 29-MAR-2001; 2001US-082317Z.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spederna SK;
 PI Padigaru M, Mishnu VS, Tchernev VT, Splek KA, Li L;
 PI Baumgartner JC, Gusev VY;
 XX
 DR WPI: 2001-639351/73.
 N-PSDB; ABA81529, ABA81530.
 XX
 PT New human G-protein coupled receptor X, GPCR, polypeptide useful in
 PT treatment or prevention of GPCR associated disorders e.g.
 PT cardiomyopathy or atherosclerosis, and to screen for antagonists and
 PT agonists useful therapeutically.
 XX
 PS Claim 1; Page 8; 157P; English.
 XX
 CC The invention relates to nucleic acid sequences (ABA81529-ABA81532) that
 CC encode G-coupled protein-receptor related polypeptides
 CC (AB44522-AB44543). The isolated polypeptide having a sequence differing
 CC by no more than 15 % of amino acid residues from one of 22 amino acid
 CC sequences (or mature forms of the sequences), fully defined in the
 CC specification and corresponding to human G-protein coupled receptor X
 CC (GPCR) polypeptides. The polypeptides have potential cardiac,
 CC antihypertensive, anabolic, cytostatic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
 CC hematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents
 CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment.
 XX
 SQ Sequence 346 AA:
 Query Match 100.0%; Score 1853; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1,5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 FOLEFMPGLILFCSFKIWSLRROQLARQARKKATRFIMVAIVITCLPSVSAR 240
 QY 241 LYLFLMTVPSSACDPVSHGALHTLSFTYNSMMDPLVYFSSPFKFNKLKISLRK 300
 Db 241 LYLFLMTVPSSACDPVSHGALHTLSFTYNSMMDPLVYFSSPFKFNKLKISLRK 300
 QY 301 QPQSKTORPEEMPISNLRGRCISVANSFOSQSDGMPHIVEMH 346
 Db 301 QPQSKTORPEEMPISNLRGRCISVANSFOSQSDGMPHIVEMH 346
 RESULT 2
 AAU06197
 ID AAU06197 standard; Protein; 346 AA.
 XX
 AC AAU06197;
 XX
 DT 19-DEC-2001 (first entry)
 XX
 DE Novel human G protein-coupled receptor (GPCR) protein.
 XX
 KM Human: G-protein coupled receptor; GPCR; chemokine receptor; protease;
 KM hyperproliferative disorder; neurological disorder; psychiatric disease;
 KW inflammatory disorder; respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200173029-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001MO-US09522.
 XX
 PR 27-MAR-2000; 2000US-192419P.
 PR 06-SEP-2000; 2000US-230459P.
 PR 20-SEP-2000; 2000US-066535.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Ye J, Cravchik A, Di Francesco V, Beasley EM;
 XX
 DR WPI: 2001-616503/71.
 N-PSDB; AAS12581.
 XX
 PT Novel human G-protein coupled receptor proteins and nucleic acid
 PT molecules encoding the protein for use in developing human therapeutics
 PT and diagnostic compositions and for identifying modulators of the
 PT protein -
 XX
 PS Claim 1; Fig 1; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC coupled receptor (GPCR) which is related to the chemokine receptor
 CC subfamily. The cDNA and gene sequences encoding for GPCR are also
 CC given in the invention. The sequences of the invention are useful
 CC for diagnosing and treating diseases or conditions mediated by human
 CC proteases. Such diseases include hyperproliferative disorders
 CC (e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease),
 CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders
 CC (e.g. diabetes) and respiratory disorders (e.g. adult respiratory
 CC distress syndrome, ARDS). The GPCR protein is also useful for identifying
 CC a modulator of the expression of the protein. It also serves as a target
 CC for identifying agents for use in mammalian therapeutic applications,
 CC e.g. a human drug, particularly modulating a biological or pathological
 CC response in a cell or tissue that expresses the protein, in biological
 CC assays related to GPCRs that are related to members of the chemokine
 CC receptor subfamily, in drug screening assays and in competition binding
 CC assays. GPCR is also useful in diagnosing a disease or predisposition to
 CC a disease mediated by the peptide, in pharmacogenomic analysis. The
 CC polynucleotide sequences can also be used in gene therapy. The present
 CC sequence represents the novel human GPCR of the invention.

SQ Sequence 346 AA; 100.0%; Score 1853; DB 22; Length 346;
 Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMTKWPSTVYLFNLAVA 60
 DB 1 MYNSCCRIEGDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMTKWPSTVYLFNLAVA 60
 QY 61 DFLMTCLEPRDYYLRRRHMAFGDIPCRVGLFTLAMNRAAGIIVVAADRYFKVYHP 120
 DB 61 DFLMTCLEPRDYYLRRRHMAFGDIPCRVGLFTLAMNRAAGIIVVAADRYFKVYHP 120
 QY 121 HHAVNTISTRAVAGIYCTLMALVILGTYLLLENHLCVQETAVSCSEFIMESANGMHDIM 180
 DB 121 HHAVNTISTRAVAGIYCTLMALVILGTYLLLENHLCVQETAVSCSEFIMESANGMHDIM 180
 QY 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 DB 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSTFTYMNMSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSTFTYMNMSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 QY 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346
 DB 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346

RESULT 3
 AA004373 standard; Protein: 346 AA.
 ID AA004373;
 AC AA004373;
 XX 23-OCT-2001 (first entry)
 DT 23-OCT-2001 (first entry)
 XX Human G-protein coupled receptor, hRUP19.
 DE Human G-protein coupled receptor; GPCR; hRUP19; agonist;
 KW Human; G-protein coupled receptor; GPCR; hRUP19; agonist;
 KM Inverse agonist; Lung cancer.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200136471-A2.
 PN WO200136471-A2.
 PD 25-MAY-2001.
 XX 16-NOV-2000; 2000MO-US31509.
 PF 16-NOV-2000; 2000MO-US31509.
 XX 17-NOV-1999; 99US-0166088.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-NOV-1999; 99US-0166369.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0195899.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.

XX (AREN-) ARENA PHARM INC.
 PA Chen R, Dang HT, Lowitz KP;
 XX WPI: 2001-355616/37.
 DR N-PSDB; AAS07946.
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 PS Claim 45; page 110-111; 160pp; English.

The sequence represents a human G-protein coupled receptor (GPCR),
 hRUP19. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. Lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

SQ Sequence 346 AA; 100.0%; Score 1853; DB 22; Length 346;
 Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMTKWPSTVYLFNLAVA 60
 DB 1 MYNSCCRIEGDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMTKWPSTVYLFNLAVA 60
 QY 61 DFLMTCLEPRDYYLRRRHMAFGDIPCRVGLFTLAMNRAAGIIVVAADRYFKVYHP 120
 DB 61 DFLMTCLEPRDYYLRRRHMAFGDIPCRVGLFTLAMNRAAGIIVVAADRYFKVYHP 120
 QY 121 HHAVNTISTRAVAGIYCTLMALVILGTYLLLENHLCVQETAVSCSEFIMESANGMHDIM 180
 DB 121 HHAVNTISTRAVAGIYCTLMALVILGTYLLLENHLCVQETAVSCSEFIMESANGMHDIM 180
 QY 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 DB 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSTFTYMNMSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSTFTYMNMSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 QY 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346
 DB 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346

RESULT 4
 AAG80968 standard; Protein: 346 AA.
 ID AAG80968;
 AC AAG80968;
 XX 28-AUG-2001 (first entry)
 DT 28-AUG-2001 (first entry)
 XX Human nGPCR1 #2.
 DE Human nGPCR1 #2.
 XX G-protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;

KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KM neuroprotective.
 XX Homo sapiens.
 OS
 PN WO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31581.
 XX
 PR 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-0166678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185542.
 PR 28-FEB-2000; 2000US-0185554.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
 PI Schellin KA, Kayles PS, Bannigan CM, Ruff V, Sejltz T, Huff RM;
 XX
 DR WPI: 2001-389826/41.
 DR N-PSDB: AAHS1008.
 XX
 PT New G protein-coupled receptor (GPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 XX
 PS Claim 37; Page 89; 261pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (GPCRs; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
 CC sequence is one such G protein-coupled receptor. GPCRs are also known as
 CC seven transmembrane receptors and function in signal transduction. The
 CC GPCR coding sequences are useful for screening a human to diagnose a
 CC disorder affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCR are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCR in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCR activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD,
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
 CC diseases e.g. inflammatory bowel disease.
 CC
 XX
 SQ Sequence 346 AA:

Query Match 100.0%; Score 1853; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCRIEGRDITISQVMPPLITVAFVLTALNGVALGCFCEPHMTKTPSTVYLFNLAVA 60
 DB 1 MYNGSCRIEGRDITISQVMPPLITVAFVLTALNGVALGCFCEPHMTKTPSTVYLFNLAVA 60
 QY 61 DFLMTICLPRFDYILRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTYVAADRYFKVYHP 120

DB 61 DFLMTICLPRFDYILRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTYVAADRYFKVYHP 120
 QY 121 HHAVENTSTRVAAGIYCTMALVYIIGTVYLLLENHLCVETAVSCSEPTMESANWHIM 180
 DB 121 HHAVENTSTRVAAGIYCTMALVYIIGTVYLLLENHLCVETAVSCSEPTMESANWHIM 180
 QY 181 FOLEFMPILGILFCSEKIVWSLRRROQLARQARKKATRFIMVVAIVITCYLPSVSR 240
 DB 181 FOLEFMPILGILFCSEKIVWSLRRROQLARQARKKATRFIMVVAIVITCYLPSVSR 240
 QY 241 LYFLMTVPSSACDPVHGALHITLFTYNSMLDPLVYFSSPEPFYKTKLCSLKP 300
 DB 241 LYFLMTVPSSACDPVHGALHITLFTYNSMLDPLVYFSSPEPFYKTKLCSLKP 300
 QY 301 QPESHKTQREEMPIISNLGRSCISVANSFQSDGQMDPHIVEH 346
 DB 301 QPESHKTQREEMPIISNLGRSCISVANSFQSDGQMDPHIVEH 346
 RESULT 5
 AAE24354
 ID AAE24354 standard; Protein; 346 AA.
 XX
 AC AAE24354;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human G protein coupled receptor (GPCR), 57242 protein.
 XX
 XX Human: G protein coupled receptor; GPCR; 57242 protein; overweight;
 KW metabolic disorder; lipogenesis; lipolysis; immunomodulator; heart;
 KW bone disorder; osteoporosis; osteogenesis; bone resorption; cachexia;
 KW hyperlipidaemia; anorexia; haematopoietic disorder; osteopathic;
 KW autoimmune disorder; psoriasis; multiple sclerosis; brain disorder;
 KW degenerative disease; Alzheimer's disease; Pick disease; diabetes;
 KW adipocyte; hyperplastic growth; hypertrophic growth; gene therapy;
 KW obesity; anorectic; receptor.
 KW
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..37
 FT /label= Signal_peptide
 FT Protein 38..346
 FT /note= "Human mature GPCR protein"
 FT Domain 1..20
 FT /note= "N-terminal non-transmembrane domain"
 FT Modified-site 3..6
 FT /note= "N-glycosylation site"
 FT Cleavage-site 9..10
 FT /note= "Cleavage site for mitochondrial preseq"
 FT Domain 21..42
 FT /note= "Transmembrane domain"
 FT Domain 32..278
 FT /note= "GPCR domain"
 FT Domain 43..51
 FT /note= "Non-transmembrane domain"
 FT Domain 52..70
 FT /note= "Transmembrane domain"
 FT Region 71..89
 FT /note= "Extracellular loop"
 FT Peptide 77..80
 FT /note= "Nuclear localisation signal"
 FT Domain 90..111
 FT /note= "Transmembrane domain"
 FT Domain 112..130
 FT /note= "Non-transmembrane domain"
 FT Domain 131..152
 FT /note= "Transmembrane domain"
 FT Region 153..184
 FT /note= "Extracellular loop"
 FT Domain 185..201

FT	/note= "transmembrane domain"
FT	Domain
FT	202..220
FT	/note= "Non-transmembrane domain"
FT	Peptide
FT	204..220
FT	/note= "Nuclear localisation signal"
FT	Modified-site
FT	216..219
FT	/note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT	Domain
FT	221..245
FT	/note= "transmembrane domain"
FT	Region
FT	245..258
FT	/note= "extracellular loop"
FT	Domain
FT	246..255
FT	/note= "Non-transmembrane domain"
FT	Domain
FT	259..280
FT	/note= "transmembrane domain"
FT	Domain
FT	281..346
FT	/note= "C-terminal cytoplasmic domain"
XX	
XX	WO200218579-A2.
PN	
PD	
PD	07-MAR-2002.
XX	
XX	29-AUG-2001; 2001MO-US26682.
PE	
PR	29-AUG-2000; 2000US-228409P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
PA	
PI	Glucksmann MA;
XX	
DR	WPI; 2002-479433/51.
DR	N-PsDB; AAD39181.
XX	
PT	Human G protein coupled receptor nucleic acid and polypeptide molecules, designated 57242, useful for diagnosing, preventing or treating aberrant lipogenesis or aberrant lipolysis, obesity, diabetes or bone disorders (e.g. osteoporosis) -
PT	
PS	Claim 9; Page 112-113; 114pp; English.
XX	
CC	The invention relates to G protein coupled receptor (GPCR) family member, 57242 and its corresponding nucleic acid sequence. The 57242 nucleic acid and polypeptide are useful for diagnosing, preventing or treating a subject having or at risk of developing a metabolic disorder, particularly a disorder associated with aberrant lipogenesis or aberrant lipolysis, obesity or diabetes. The 57242 DNA and protein are also useful for treating a subject having bone disorder, where the disorder is osteoporosis or a disorder associated with aberrant osteogenesis or aberrant bone resorption. These diseases include obesity, diabetes, hyperlipidaemia, overweight, anorexia or cachexia.
CC	The 57242 DNA and protein are also useful for treating a subject having haematopoietic disorders, autoimmune disorders e.g. psoriasis and multiple sclerosis, brain disorders, degenerative diseases e.g. Alzheimer's disease and Pick disease and disorders involving heart.
CC	The 57242 nucleic acid and polypeptide are also useful for modulating adipocyte activity such as hyperplastic growth, hypertrophic growth or lipogenesis. The 57242 DNA is used in gene therapy. The present sequence is human 57242 protein.
CC	
XX	
SQ	Sequence 346 AA;
Query Match	100.0%; Score 1853; DB 23; Length 346;
Best Local Similarity	100.0%; Pred. No. 1.5e-199;
Matches 346;	Conservative 0; Mismatches 0; Indels 0; Gaps
OY	1 MYNSCCRIEGDITISVMPPLIVAFVIGALNGVALCGFCFHKMTWKSPSTVIFENLAVA 60 Db
D	1 MYNSCCRIEGRDISVMPPLIVAFVIGALNGVALCGFCFHKMTWKSPSTVIFENLAVA 60 OY
D	61 DELLMLICLPRTDYILARRRHMAAGDIPCAVGFLTLANMRAGSIVFLTVAADRFKVVHP 120 61 DFLMLICLPRTDYILARRRHMAAGDIPCAVGFLTLANMRAGSIVFLTVAADRFKVVHP 120

OY	121	HHNNTSTRAGAVTCTMALVLTCTVYLLLENHICVQETAVSCEPSFIMSANGMDIM	180
OY	121	HHNNTSTRAGAVTCTMALVLTCTVYLLLENHICVQETAVSCEPSFIMSANGMDIM	180
Db	121	HHAVNTSTRAGAVTCTMALVLTCTVYLLLENHICVQETAVSCEPSFIMSANGMDIM	180
OY	181	FQLEFFNPDLGITLFCSPKRWLSLRRRQQLARQARKKATRFIMVAIVFIFTCYLPVSAR	240
Db	181	FQLEFFNPDLGITLFCSPKRWLSLRRRQQLARQARKKATRFIMVAIVFIFTCYLPVSAR	240
OY	241	LYFLMTVPSSACDPVSAGALHTLTLSTYNNSMLDPLVYFESSPSFPEKYNKLTCSLKP	300
Db	241	LYFLMTVPSSACDPVSAGALHTLTLSTYNNSMMDPLVYFESSPSFPEKYNKLTCSLKP	300
OY	301	QPGSKTORPEEMPISMLGRRSCISVANSFQSGDSQGMPHIVEWH	346
Db	301	QPGSKTORPEEMPISMLGRRSCISVANSFQSGDSQGMPHIVEWH	346
RESULT	6		
AA014788			
ID	AA014788	standard; Protein; 346 AA.	
XX	AA014788:		
AC			
XX			
D7	28-JUN-2002	(first entry)	
XX			
DE		Human purinergic-like G-protein coupled receptor (AXOR87).	
XX			
KW		Human; purinergic-like G-protein coupled receptor; AXOR87; immunity;	
KW		autoimmunity; inflammation; immunodeficiency; bacterial infection;	
KW		fungal infection; viral infection; protozoa infection; cancer; diabetes;	
KW		obesity; anorexia; bulimia; asthma; psoriasis; rheumatoid arthritis;	
KW		osteoarthritis; psychotic disorder; neurological disorder; vaccine;	
XX		chromosome 12q24.	
XX			
OS		Homo sapiens.	
PN	GB2365868-A.		
PD	27-FEB-2002.		
XX			
PE	25-MAY-2001; 2001GB-0012860.		
PR	30-MAY-2000; 2000US-0580675.		
PR	02-NOV-2000; 2000GB-0026839.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
PA	(GLAX) GLAXO GROUP LTD.		
XX			
PI	Ignar DM, Elshourbagy N, Gattu M, Shabon U;		
XX			
DR	WPI; 2002-364852/40.		
DR	N-PSDB; AAL42499.		
XX			
PT	New purinergic-like G-protein coupled receptor AXOR87 polypeptide and		
PT	polynucleotide, useful for treating diseases related to autoimmunity,		
PT	inflammation, immunodeficiency, or bacterial, fungal, viral and		
PT	protozoal infections		
XX			
PS	Claim 2; Page 36; 47pp: English.		
XX			
XX			
CC	The invention comprises the amino acid and coding sequence of the human		
CC	purinergic-like G-protein coupled receptor AXOR87. The AXOR87 DNA and		
CC	protein sequences of the invention may be used for treating diseases		
CC	related to immunity, autoimmunity, inflammation, immunodeficiency, and		
CC	infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA and		
CC	protein sequences are particularly useful for treating: cancers,		
CC	diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid		
CC	arthritis, osteoarthritis, as well as psychotic and neurological		
CC	disorders. The AXOR87 DNA and protein sequences may also be used as		
CC	vaccines. The present amino acid sequence (encoded by a sequence located		
CC	on chromosome 12q24) represents the human AXOR87 protein.		

XX Sequence 346 AA;
 SQ Query Match 100.0%; Score 1853; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIVAFVIGALGNGVALCGCFCHMKTKPSTVYLENLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIVAFVIGALGNGVALCGCFCHMKTKPSTVYLENLAVA 60
 QY 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 DB 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 QY 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPLGIIILFCSEFKIYWSLRRQOLARQARKKATREIMVVAIVETTCYLPVSAR 240
 DB 181 FOLEFEMPLGIIILFCSEFKIYWSLRRQOLARQARKKATREIMVVAIVETTCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVHGALHITLSTFYMNSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 DB 241 LYFLMTVPSSACDPVHGALHITLSTFYMNSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346

RESULT 7
 ABB08596
 ID ABB08596 standard; Protein: 346 AA.
 AC ABB08596;
 DT 01-JUL-2002 (first entry)
 XX
 DE Human lipocyte-originated G protein-coupled receptor protein TGR13.
 XX
 KW Antinflammatory; anorectic; obesity; inflammation; gene therapy;
 KW human; G protein-coupled receptor protein TGR13.
 XX
 OS Homo sapiens.
 PN WO200202767-A1.
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-JP05711.
 XX
 PR 04-JUL-2000; 2000JP-0206860.
 PR 31-JUL-2000; 2000JP-0235274.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Shibata S, Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;
 DR WPI; 2002-164535/21.
 DR N-PSDB; ABA99236.
 XX
 PT New human lipocyte-originated G protein-coupled receptor proteins TGR13
 PT and encoding DNAs, for developing drugs to treat obesity and
 PT inflammation, including gene therapy
 XX
 PS Claim 1; Fig 2; 101pp; Japanese.
 CC This invention relates to a human lipocyte-originated G protein-coupled
 CC receptor proteins TGR13, thought to be antinflammatory and anorectic in
 CC their action. The proteins and encoded DNAs are for use in developing
 CC drugs to treat obesity and inflammation, including gene therapy.
 QC

CC The present sequence represents the human lipocyte-originated G
 CC protein-coupled receptor protein TGR13.
 XX
 SQ Sequence 346 AA;
 SQ Query Match 100.0%; Score 1853; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIVAFVIGALGNGVALCGCFCHMKTKPSTVYLENLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIVAFVIGALGNGVALCGCFCHMKTKPSTVYLENLAVA 60
 QY 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 DB 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 QY 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPLGIIILFCSEFKIYWSLRRQOLARQARKKATREIMVVAIVETTCYLPVSAR 240
 DB 181 FOLEFEMPLGIIILFCSEFKIYWSLRRQOLARQARKKATREIMVVAIVETTCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVHGALHITLSTFYMNSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 DB 241 LYFLMTVPSSACDPVHGALHITLSTFYMNSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346

RESULT 8
 AAE16172
 ID AAE16172 standard; Protein: 346 AA.
 AC AAE16172;
 DT 26-MAR-2002 (first entry)
 XX
 DE Human G-protein coupled receptor 3 (GCRHC-3) protein.
 XX
 KW Human; G-protein coupled receptor 3; cell proliferative disorder;
 KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
 KW gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
 KW acquired immune deficiency syndrome; inflammatory disorder; infection;
 KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
 KW diabetes; obesity; osteoporosis; gene therapy; GCRHC-3.
 XX
 OS Homo sapiens.
 PN
 PD
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..32
 FT /label= Signal_peptide
 FT 33..346
 FT Protein
 FT /label= Human_mature_GCRHC-3_Protein
 FT Domain 20..44
 FT /note= "Transmembrane domain"
 FT 93..110
 FT /note= "Transmembrane domain"
 FT Domain 137..154
 FT /note= "Transmembrane domain"
 FT 222..244
 FT /note= "Transmembrane domain"
 XX
 PN WO200187937-A2.
 XX 22-NOV-2001.
 PD

PF 17-MAY-2001; 2001WO-US16285.
 XX
 PR 18-MAY-2000; 2000US-205628P.
 PR 22-MAY-2000; 2000US-206222P.
 PR 25-MAY-2000; 2000US-207566P.
 PR 02-JUN-2000; 2000US-208834P.
 PR 02-JUN-2000; 2000US-208861P.
 XX
 PA (INCYTE GENOMICS INC.
 XX
 PI Patterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R;
 PI Khan FA, Gandhi AR, Wajia NK, Nguyen DB, Yue H, Hafalia A;
 PI Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;
 XX
 DR WPI: 2002-089844/12.
 DR N-PSDB: AAD26371.
 XX
 PT Novel G-protein coupled receptors and polynucleotides useful for
 PT diagnosis, treatment and prevention of disorders of cell proliferation,
 PT neurological, cardiovascular, metabolic disorders and viral infections
 XX
 PS Claim 1; Page 105-106; 115pp; English.
 XX
 CC The invention relates to human G-protein coupled receptor (GPCR)
 CC polypeptides and polynucleotides. GPCR polypeptides are useful for
 CC screening compounds that modulate their activity. They are useful in
 CC the diagnosis, prevention and treatment of disorders which include
 CC cell proliferative disorders such as arteriosclerosis, hepatitis,
 CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukemia,
 CC lymphoma; neurological disorders such as epilepsy, ischemic
 CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
 CC Parkinson's disease, ataxia, multiple sclerosis, bacterial and viral
 CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
 CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
 CC hypertension, vascular tumours, myocardial infarction, hypertensive
 CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;
 CC gastrointestinal disorders such as dysphagia, peptic oesophagitis;
 CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
 CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
 CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
 CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
 CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
 CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
 CC fungal, parasitic, protozoal and helminthic infections and trauma;
 CC metabolic disorders such as diabetes, obesity and osteoporosis; and
 CC viral infections such as infection caused by viral agent classified as
 CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention
 CC are useful as probes for assessing toxicity of test compounds. They are
 CC also used in gene therapy. The present sequence is human G-protein
 CC coupled receptor 3 (GCR3-3) protein.
 CC
 XX
 SQ Sequence 346 AA;
 Query Match 100.0%; Score 1853; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYNGSCRIEPTISQVMPPLIVAFVIGALGNGVALGCFCHMTKRWKSTYLLNLA 60
 DB 1 MYNGSCRIEPTISQVMPPLIVAFVIGALGNGVALGCFCHMTKRWKSTYLLNLA 60
 QY 61 DELLMLICLFFRDYVLLRRHMAFGDIPCRVGLFTLAMNAGSIVELTVAAADRYKVVHP 120
 DB 61 DELLMLICLFFRDYVLLRRHMAFGDIPCRVGLFTLAMNAGSIVELTVAAADRYKVVHP 120
 QY 121 HHAVENTISRVAGIVCTMAVYLLIGTYVLLLENHLCOVETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAVENTISRVAGIVCTMAVYLLIGTYVLLLENHLCOVETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFPMGLILFCSEFKVWSLRRQOLARQARKKATRTMVAIVETITCLPSVSAR 240
 DB 181 FOLEFPMGLILFCSEFKVWSLRRQOLARQARKKATRTMVAIVETITCLPSVSAR 240

DB 181 FOLEFPMGLILFCSEFKVWSLRRQOLARQARKKATRTMVAIVETITCLPSVSAR 240
 QY 241 LYELMTVPSSACDPVSHGALHTITSEYTNNSMLDPLVYFESSPPKPFYKIKISLMPK 300
 DB 241 LYELMTVPSSACDPVSHGALHTITSEYTNNSMLDPLVYFESSPPKPFYKIKISLMPK 300
 QY 301 OPGHSTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
 DB 301 OPGHSTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
 RESULT 9
 AA011401
 ID AA011401 standard; Protein; 346 AA.
 XX
 AC AA011401;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE HM74-like G-protein coupled receptor (GPCR).
 XX
 KW HM74-like GPCR: G-protein coupled receptor; antibacterial; fungicide;
 KW protozoacide; analgesic; cytotatic; neuroleptic; nootropic;
 KW anticonvulsant; tranquiliser; viral infection; pain; cancer; anorexia;
 KW bulimia; asthma; central nervous system disease; CNS disease;
 KW cardiovascular disease; hypotension; hypertension; angina pectoris;
 KW myocardial infarction; urinary retention; osteoporosis; ulcer; asthma;
 KW inflammatory disorder; benign prostatic hypertrophy; multiple sclerosis;
 KW psychotic disorder; neurological disorder; dyskinesia;
 KW Huntington's disease; Tourette's syndrome; anxiety; schizophrenia;
 KW manic depression; delirium; dementia; mental retardation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Domain 20..37
 FT /label= Transmembrane_domain_1
 FT Domain 53..73
 FT /label= Transmembrane_domain_2
 FT Domain 91..113
 FT /label= Transmembrane_domain_3
 FT Domain 133..150
 FT /label= Transmembrane_domain_4
 FT Domain 180..197
 FT /label= Transmembrane_domain_5
 FT Domain 223..242
 FT /label= Transmembrane_domain_6
 FT Domain 260..279
 FT /label= Transmembrane_domain_7
 FT Region 101..118
 FT /label= GPCR-region
 FT /note= "G-protein coupled receptor region"
 FT
 PN WO200177320-A2.
 XX
 PD 18-OCT-2001.
 XX
 PP 04-APR-2001; 2001WO-EP03811.
 XX
 PR 05-APR-2000; 2000US-194701P.
 XX
 PA (FAR) BAYER AG.
 XX
 PI Xiao Y;
 XX
 DR WPI: 2002-049147/06.
 DR N-PSDB: AAS18501.
 XX
 PT Novel isolated polynucleotide, useful for treating infection, pain,
 PT cancer, asthma, hypertension, myocardial infarction, urinary retention,
 PT osteoporosis, encodes the human HM74-like G-protein coupled receptor
 PT polypeptide

PS Claim 1; Fig 2; 77pp; English.

XX The invention describes a novel isolated polynucleotide (I) encoding a
CC human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents
CC that regulate HM74-like GPCR are useful for modulating the activity of
CC the protein in a disease selected from bacterial, fungal, protozoan, and
CC viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous
CC system (CNS) disease, cardiovascular disease, hypotension, hypertension,
CC angina pectoris, myocardial infarction, urinary retention, osteoporosis,
CC ulcer, asthma, inflammation, allergy, benign prostatic hyper trophy,
CC multiple sclerosis and dyskinesia such as Huntington's disease and
CC Tourette's syndrome. The composition is also useful for treating
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, delirium, dementia and severe mental retardation. (I)
CC the HM74-like GPCR polypeptide are also useful for treating the above
CC mentioned diseases. (I) is useful in a diagnostic assay for detecting
CC diseases, susceptibility to diseases and abnormalities related to the
CC presence of mutations in the nucleic acid sequences which encode a GPCR.
CC The polypeptide is useful to identify test compounds which may act as
CC agonists or antagonists at the receptor site and which can be regulated
CC to provide therapeutic effects. The polypeptide is also useful as a bait
CC protein in a two-hybrid or three-hybrid assay, and to immunise a mammal
CC for production of polyclonal antibodies. This the amino acid sequence of
CC human HM74-like GPCR described in the method of the invention.

XX Sequence 346 AA:

Query Match 100.0%; Score 1853; DB 23; Length 346;

Best Local Similarity 100.0%; Pred. No. 1.5e-199; Mismatches 0; Gaps 0;

Matches 346; Conservative 0; Indels 0; Gaps 0;

OY 1 MYNGSCRIEGDITISQVMPPLIYAFVLAGALNGVALGCFEPMKPTVYLENLAVA 60
DB 1 MYNGSCRIEGDITISQVMPPLIYAFVLAGALNGVALGCFEPMKPTVYLENLAVA 60
OY 61 DFLMILICPFRDYLRHRRHAFGDIIPCRVGLFTLNNRAGSIYFLVYVADRFKXVHP 120
DB 61 DFLMILICPFRDYLRHRRHAFGDIIPCRVGLFTLNNRAGSIYFLVYVADRFKXVHP 120
OY 121 HNAVNTISTRVAGIVCTLMALVILGTVYLLLENHLQVQFVAVSCSEFIMESANGMDIM 180
DB 121 HNAVNTISTRVAGIVCTLMALVILGTVYLLLENHLQVQFVAVSCSEFIMESANGMDIM 180
OY 181 FOLEFFMPLGILFCSEKIWSLRROOLARQARKKATRFIMVAVIFICYLPVSAR 240
DB 181 FOLEFFMPLGILFCSEKIWSLRROOLARQARKKATRFIMVAVIFICYLPVSAR 240
OY 241 LYELMTVSSACDPVHGLHTLTSFTYMNMSMLDPLVYFSSPPKRYNKLKICSLPK 300
DB 241 LYELMTVSSACDPVHGLHTLTSFTYMNMSMLDPLVYFSSPPKRYNKLKICSLPK 300
OY 301 OPGHSKTORPEEMPIISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346
DB 301 OPGHSKTORPEEMPIISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346

RESULT 10

AAEI1077
ID AAEI1077 standard; Protein: 346 AA.

XX AAEI1077;

XX 18-APR-2002 (first entry)

DE Human G-protein coupled receptor (GPCRx14) protein.

XX Human: G-protein coupled receptor: GPCRx14; cerebroprotective; vomiting;
KM receptor-mediated disorder: therapy; urinary retention; allergy; obesity;
KM osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
KM anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;
KM stroke; hypertension; neuronal disorder; myocardial infarction psychotic;
KM depression; mental retardation; neurodegenerative disease; antibacterial;
KM Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;

KM Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
KM vulnerable; analgesic; anorectic; anabolic; diuretic; cardiant; nootropic;
KM antileptic; vasotropic; diabetes; cancer; tranquillizer; neuroleptic.

OS Homo sapiens.

XX Key

Location/Qualifiers

FT Domain

/note= "Transmembrane domain"

FT Domain

/note= "Transmembrane domain"

FT Domain

/note= "Transmembrane domain"

FT Domain

/note= "Transmembrane domain"

FT Domain

/note= "Transmembrane domain"

FT Domain

/note= "Transmembrane domain"

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QY 1 MYNSCCRIEEDTISQVMPPLIIAFAVLGANGVALCGFCFHKMTWKPSVYLFNLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIIAFAVLGANGVALCGFCFHKMTWKPSVYLFNLAVA 60
 QY 61 DFLMILCPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFLTVAADRFKVVHP 120
 DB 61 DFLMILCPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFLTVAADRFKVVHP 120
 QY 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPGLIILFCSEFRIWMSLRROQLAQAAMKATRFIMVVAIVFTTCYLPVSAR 240
 DB 181 FOLEFEMPGLIILFCSEFRIWMSLRROQLAQAAMKATRFIMVVAIVFTTCYLPVSAR 240
 QY 241 LYFLMTVSSACDPSVHGALHITLSFTYMSMDPLVYSSSPFKEYKIKICSLKPK 300
 DB 241 LYFLMTVSSACDPSVHGALHITLSFTYMSMDPLVYSSSPFKEYKIKICSLKPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346
 DB 301 QPGHSKTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346

RESULT 11
 ID ABB44523 standard; Protein: 346 AA.
 XX ABB44523;
 AC ABB44523;
 DT 28-JAN-2002 (first entry)
 XX Human GPCR1C polypeptide SEQ ID NO 5.
 DE Human: GPCR1C polypeptide; cardiant; antiarteriosclerotic;
 KW anabolic; cytosolic; antiviral; gene therapy; cardiomyopathy; obesity;
 KW asthma; Alzheimer's disease; Crohn's disease; multiple sclerosis;
 KW infection; human immunodeficiency virus; HIV.
 XX OS Homo sapiens.
 XX WO200174904-A2.
 XX 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US10241.
 PF 31-MAR-2000; 2000US-193664P.
 PR 05-APR-2000; 2000US-194614P.
 PR 06-APR-2000; 2000US-195063P.
 PR 06-APR-2000; 2000US-195066P.
 PR 06-APR-2000; 2000US-195067P.
 PR 06-APR-2000; 2000US-195068P.
 PR 06-APR-2000; 2000US-195069P.
 PR 06-APR-2000; 2000US-195070P.
 PR 21-JUL-2000; 2000US-219855P.
 PR 27-JUL-2000; 2000US-221284P.
 PR 28-JUL-2000; 2000US-221325P.
 PR 11-AUG-2000; 2000US-224588P.
 PR 11-OCT-2000; 2000US-239613P.
 PR 18-JAN-2001; 2001US-262508P.
 PR 23-JAN-2001; 2001US-263433P.
 PR 23-JAN-2001; 2001US-263604P.
 PR 30-JAN-2001; 2001US-265161P.
 PR 29-MAR-2001; 2001US-0823172.
 XX (CURA-) CURAGEN CORP.
 PA Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;
 PI Padigaru M, Mishu VS, Tchernev VT, Spytek KA, Li L;

PI Baumgartner JC, Gusev VY;
 XX WPI: 2001-639351/73.
 DR N-PSDB; ABA81531.
 XX New human G-protein coupled receptor X, GPCR-X, polypeptide useful in
 PT treatment or prevention of GPCR-X associated disorders e.g.
 PT cardiomyopathy or atherosclerosis, and to screen for antagonists and
 PT agonists useful therapeutically
 XX Claim 1; Page 11; 157pp; English.

The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
 encode G-coupled protein-receptor related polypeptides
 (ABA44522-ABA44543). The isolated polypeptide having a sequence differing
 by no more than 15 % of amino acid residues from one of 22 amino acid
 sequences (or mature forms of the sequences), fully defined in the
 CC specification and corresponding to human G-protein coupled receptor X
 CC (GPCR-X) polypeptides. The polypeptides have potential cardiant,
 CC antiarteriosclerotic, anabolic, cytosolic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-X-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease), immune disorders,
 CC haematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents
 CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment.

Sequence 346 AA:
 SQ

Query Match 99.2%; Score 1839; DB 22; Length 346;
 Best Local Similarity 99.4%; Pred. No. 5.6e-198;
 Matches 344; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIIAFAVLGANGVALCGFCFHKMTWKPSVYLFNLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIIAFAVLGANGVALCGFCFHKMTWKPSVYLFNLAVA 60
 QY 61 DFLMILCPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFLTVAADRFKVVHP 120
 DB 61 DFLMILCPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFLTVAADRFKVVHP 120
 QY 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPGLIILFCSEFRIWMSLRROQLAQAAMKATRFIMVVAIVFTTCYLPVSAR 240
 DB 181 FOLEFEMPGLIILFCSEFRIWMSLRROQLAQAAMKATRFIMVVAIVFTTCYLPVSAR 240
 QY 241 LYFLMTVSSACDPSVHGALHITLSFTYMSMDPLVYSSSPFKEYKIKICSLKPK 300
 DB 241 LYFLMTVSSACDPSVHGALHITLSFTYMSMDPLVYSSSPFKEYKIKICSLKPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346
 DB 301 QPGHSKTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346

RESULT 12
 ID AAG80934
 ID AAG80934 standard; Protein: 296 AA.

XX AAG80934;
 AC
 XX
 DT 28-AUG-2001 (first entry)
 DE
 XX Human ngPCR11 #1.
 XX
 DE G protein-coupled receptor; ngPCR; seven transmembrane receptor;
 XX signal transduction; schizophrenia; thyroid disorder; renal failure;
 XX rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective.
 OS Homo sapiens.
 XX
 PN WO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31581.
 XX
 PR 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-0166678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185554.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PHRA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogeli G, Wood LS, Parodi IA, Hiesch RR, Lind P, Slightom J;
 PI Schellin KA, Kayles PS, Bannigan CM, Ruff V, Sejlitz T, Ruff RM;
 XX WPI: 2001-389826/41.
 XX N-PSDB; AAH50974.
 DR
 XX
 PT New G protein-coupled receptor (ngPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 PS Claim 37; Pages 77-78; 261pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (ngPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
 CC sequence is one such G protein-coupled receptor. GPCR's are also known as
 CC seven transmembrane receptors and function in signal transduction. The
 CC ngPCRx coding sequences are useful for screening a human to diagnose a
 CC disorder affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. ngPCRx are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of ngPCRx in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of ngPCRx activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
 CC diseases e.g. inflammatory bowel disease.
 XX
 XX
 SQ Sequence 296 AA:
 Query Match 84.7%; Score 1570; DB 22; Length 296;
 Best Local Similarity 100.0%; Pred. No. 8.2e-168;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21 LLVAEVLGALGVALGCGFPMKTKWPSYVLLFNLAVADFLMCLPFRDYLLRRH 80
 DB 1 LLVAEVLGALGVALGCGFPMKTKWPSYVLLFNLAVADFLMCLPFRDYLLRRH 60
 OY 81 WAFGDIPCRYGFTLLAMNRAGSIVFLVVAADRYFKVVRPHNAVNTISFVAGIVCTLM 140
 DB 61 WAFGDIPCRYGFTLLAMNRAGSIVFLVVAADRYFKVVRPHNAVNTISFVAGIVCTLM 120
 OY 141 ALVILGTVLLLENHLCVQETAVSCSFIMESANGHNDIMFQLEFPMPLGILLFCSFKIV 200
 DB 121 ALVILGTVLLLENHLCVQETAVSCSFIMESANGHNDIMFQLEFPMPLGILLFCSFKIV 180
 OY 201 WSLRRQQLARQARMKKATPEIMVAIVFTCYLPSVARSALYELMTVPSSACDPVHGAL 260
 DB 181 WSLRRQQLARQARMKKATPEIMVAIVFTCYLPSVARSALYELMTVPSSACDPVHGAL 240
 OY 261 HTPLSFTYNSMDPLVYFSSSPFKFYNNKIKICSLKPKQDSKTQRPDEMPIS 316
 DB 241 HTPLSFTYNSMDPLVYFSSSPFKFYNNKIKICSLKPKQDSKTQRPDEMPIS 296
 RESULT 13
 AAU77992 standard; Protein; 387 AA.
 XX
 ID AAU77992;
 XX
 AC AAU77992;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human Inflammation-associated GPCR EX20 polypeptide.
 XX
 KW Human: inflammation-associated G-protein coupled receptor; GPCR; EX20;
 KW inflammatory disease; asthma; adult respiratory distress syndrome; ARDS;
 KW chronic obstructive pulmonary disease; COPD; bronchitis; emphysema;
 KW pneumoconiosis; neutrophil; eosinophil related disorder; allergy;
 KW lung-related disorder; rheumatoid arthritis; inflammatory bowel disease;
 KW ulcerative colitis; skin disease; eczematous dermatitis; receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200213845-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 16-AUG-2001; 2001WO-EP09466.
 XX
 PR 18-AUG-2000; 2000US-0641653.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PI Jaraal G, Yousefi S;
 XX WPI: 2002-329542/36.
 XX N-PSDB; ABK47759.
 DR
 XX
 PT New pharmaceutical composition comprising EX20 polypeptide, EX20
 PT polynucleotide, antibodies against EX20 polypeptide, antisense
 PT oligonucleotides against EX20 polynucleotide, useful for treating
 PT inflammatory disease -
 XX
 PS Claim 2; Page 31-32; 36pp; English.
 XX
 CC The present invention relates to human inflammation-associated

PN WO200136471-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31509.
 XX
 PR 17-NOV-1999; 99US-0166088.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-NOV-1999; 99US-0166369.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 11-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210982.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Dang HT, Lowitz KP;
 XX
 DR WPI: 2001-355616/37.
 N-PSDB: AAS07952.
 XX
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX
 PS Claim 69; Page 121-122; 160pp; English.
 XX
 CC The sequence represents a human G-protein coupled receptor (GPCR),
 CC hRUP25. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilised to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX
 SO Sequence 363 AA:
 Query Match 47.7%; Score 883.5; DB 22; Length 363;
 Best Local Similarity 52.8%; Pred. No. 1.8e-90;
 Matches 180; Conservative 47; Mismatches 107; Indels 7; Gaps 4;
 QY 5 SCCRIIGDIIISOVMEPLLIVAFVLGALNGVALGCFPHMKTWKPSTYLENLAVADFL 64
 DB 17 NCCVFEDDPIVAVLPVLGLFEFLGGLNGLAMITCFHLKSKSRIFLENLAVADFL 76
 QY 65 MCLPFRDYLLRRHMAFGDIPCRVGLFTLMMNRAGSIIVFLVVAADYERKVPHPHAY 124
 DB 77 IICLPFLMDNYRRMWRKFGDIPCRMLFPLMMNRGSIIFLVVAADYERKVPHPHAY 136
 QY 125 NITSTVAAAGIVCTMALVILGTVILLNLCVOETAVSCSFIMESANGWHDIMFQLE 184
 DB 137 NKISNTAAIISCLMGIITGLTVHLKKMPIONGANICSSFSICHTFQWHEAMFLE 196
 QY 185 FEMPELIIIFCSFKIYWSBRQOLARQAMKATFEIVVAIVFTCYLPSVARIYFL 244
 DB 197 FELPLIILFCSARIISLQR-OMDRHAKIKRAITFEIVVAIVFVFCPLPSVVVRIIE 255

QY 245 WTVPSA---CD--PSVHGAHITLSEFYWNSMLDPLVYFFSSSPKFEYNKLIKCSLKP 299
 DB 256 WLHTSGTQNCVEYRSVDLAFITLSEFYWNSMLDPLVYFFSSSPKFEYNKLIKCSL 315
 QY 300 KOPGSKTQRPPEMPISNLGRSCISVANSFQSDGQMDP 340
 DB 316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPMSP 355
 Search completed: March 26, 2003, 19:37:33
 Job time : 77 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:36:29 ; Search time 29 Seconds
(without alignments)
351.046 Million cell updates/sec

Title: US-09-942-374-2
Perfect score: 1853
Sequence: 1 MYN5GCRIRGDRISQVMP.....ANSFQSDGQMPHIYEMH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCRU8.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	28.5	423	2	US-08-955-713-2
2	510	27.5	476	2	US-08-955-713-4
3	451.5	24.4	319	3	US-09-130-749-2
4	451.5	24.4	319	3	US-09-130-749-2
5	371	20.0	362	3	US-08-513-974B-374
6	362.5	19.6	373	2	US-08-555-524A-4
7	362.5	19.6	373	3	US-08-749-707-4
8	346.5	18.7	370	3	US-08-781-250-2
9	336	18.1	339	2	US-08-153-848-4
10	336	18.1	339	2	US-08-812-871-3
11	336	18.1	339	3	US-09-299-843A-44
12	336	18.1	339	4	US-09-088-337B-44
13	336	18.1	339	5	PCT-US93-11153-44
14	336	18.1	339	5	PCT-US95-07180-2
15	328.5	17.7	302	2	US-08-467-948A-30
16	328.5	17.7	302	2	US-08-467-947A-30
17	327	17.6	309	4	US-09-422-869-20
18	325	17.5	344	2	US-08-467-948A-8
19	325	17.5	344	3	US-08-467-947A-8
20	314	16.9	334	3	US-08-513-974B-373
21	308	16.6	325	1	US-08-118-270-51
22	308	16.6	325	5	PCT-US93-08528-51
23	307	16.6	391	1	US-07-816-283-4
24	307	16.6	391	1	US-08-417-103-4
25	307	16.6	395	1	US-08-097-958-5
26	307	16.6	395	1	US-08-476-000-5
27	307	16.6	395	1	US-08-472-840-5

28	307	16.6	395	2	US-08-476-976-5	Sequence 5, Appl1
29	307	16.6	395	3	US-08-474-410-5	Sequence 5, Appl1
30	306	16.5	398	1	US-08-097-938-6	Sequence 6, Appl1
31	306	16.5	398	1	US-08-476-000-6	Sequence 6, Appl1
32	306	16.5	398	1	US-08-472-840-6	Sequence 6, Appl1
33	306	16.5	398	2	US-08-476-976-6	Sequence 6, Appl1
34	306	16.5	398	3	US-08-474-410-6	Sequence 6, Appl1
35	306	16.5	398	4	US-08-486-673B-6	Sequence 6, Appl1
36	305.5	16.5	369	4	US-08-120-601B-9	Sequence 9, Appl1
37	305.5	16.5	391	1	US-07-816-283-2	Sequence 2, Appl1
38	305.5	16.5	391	1	US-08-417-103-2	Sequence 2, Appl1
39	305.5	16.5	391	1	US-08-417-103-14	Sequence 14, Appl1
40	305	16.5	337	4	US-09-044-404A-2	Sequence 2, Appl1
41	303.5	16.4	391	4	US-08-120-601B-8	Sequence 8, Appl1
42	302.5	16.3	369	1	US-07-816-283-6	Sequence 6, Appl1
43	302.5	16.3	369	1	US-08-417-103-6	Sequence 6, Appl1
44	302.5	16.3	369	1	US-08-417-103-16	Sequence 16, Appl1
45	302	16.3	364	4	US-08-148-708-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5955308
GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMAN, DEK
; APPLICANT: HALSEY, WENDY
TITLE OF INVENTION: CDNA CLONE HEODS4 THAT ENCODES A HUMAN 7-TRANS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955, 713
FILING DATE: 23-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,124
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70087
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-955-713-2
Query Match 28.5%; Score 529; DB 2; Length 423;
Best Local Similarity 39.2%; Pred. No. 3.9e-38;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

Db 6 CSAPSTVATVAVGVLLGECGLGILLGNAAVAMTFLEFRVRVWKPYAVYLLNALADLLAA 65
QY 67 CLPFRDYYLRRRMAFGDIPCRVGLFTLAMNAGSIVLTVVAADRYFKVPHHNAVNT 126
Db 66 CLPFLAFTLSQAMHLGRVGMALRFLDLRSVGMFLAAVALDRRLRVHRLKYNL 125
QY 127 ISTRVAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANG----WHDIME 181
Db 126 LSPQALGVSGVLVLMALVITCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIQOALIS 182
QY 182 QLEFMPGLIILFCSEFKIYWSLRR--QQLARQARKKATRFIMVAIVITCYLPSVSAR 240
Db 183 CLQFVLPFGILVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVLFCPLCPCLAR 242
QY 241 --LYFLMTVPSSACDPVSGALHITLFTYMSMDLPVYFSSPFPKYNKL 292
Db 243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSLVNPVYVCFSSPFRSSYRNV 296

RESULT 4
US-09-130-749-2

; Sequence 2, Application US/09130749
; Patent No. 6031344
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; TITLE OF INVENTION: RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-130-749-2

Query Match

Best Local Similarity 24.4%; Score 451.5; DB 3; Length 319;
Matches 101; Conservative 61; Mismatches 121; Indels 11; Gaps 5;

QY 7 CRIGEDTISQVMPPLIYAFVGLAGVAGLGCFCFHMKTTPKSTVYVLFNLNAVDLLMI 66
Db 6 CSAPSTVATVAVGVLLGECGLGILLGNAAVAMTFLEFRVRVWKPYAVYLLNALADLLAA 65

QY 67 CLPFRDYYLRRRMAFGDIPCRVGLFTLAMNAGSIVLTVVAADRYFKVPHHNAVNT 126
Db 66 CLPFLAFTLSQAMHLGRVGMALRFLDLRSVGMFLAAVALDRRLRVHRLKYNL 125
QY 127 ISTRVAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANG----WHDIME 181
Db 126 LSPQALGVSGVLVLMALVITCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIQOALIS 182
QY 182 QLEFMPGLIILFCSEFKIYWSLRR--QQLARQARKKATRFIMVAIVITCYLPSVSAR 240
Db 183 CLQFVLPFGILVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVLFCPLCPCLAR 242
QY 241 --LYFLMTVPSSACDPVSGALHITLFTYMSMDLPVYFSSPFPKYNKL 292
Db 243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSLVNPVYVCFSSPFRSSYRNV 296

RESULT 5
US-08-513-974B-374

; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION DATA:


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APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34, 235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-374

```

```

Query Match          20.0% Score 371; DB 3; Length 362;
Best Local Similarity 29.1% Pred No. 1.4e-24;
Matches 95; Conservative 60; Mismatches 128; Indels 44; Gaps 7;

```

```

QY 18 MPPLIIVAVLGAINGVALGCGFCFHKMTKPSVYLFENLAVADFLIMICLPRTDYLR 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 43 LPVYILVFTIGFGLGNSVAIIMFVFMHMPGSIYVFNALADFLYVLPALFYFN 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 RRHAFDIPCRVGLFTLMMNRAGSIVFLVVAADRFKVVPHHNAVNTSTVNAAGIYC 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 103 KIDWIFGDWCKLQRFIFHNLYGSLFLTCISAHRYSGVYPLKSGRLKKNAYISV 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 138 TLMALVILGTYYLLLEHNL-----CVQETA-----VSCSEFIMESANGMHD 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 163 LVMALVAVAIAPILFYSIGVGRNKTITCYDTADEYLRSFYVSMCTVFN----- 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 IMFQLEFMPGLILFCSEFKIWSLRRQOLARQARMKATRFIMVAIVFTCYLP--- 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 -----FCIPFTIILGCGYILVAKALYK-DLDSNPLRRKSTVILVLFVAVSYLPHV 267
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 ----SVSATLYFLMTVPSSACDPVHGALHTLSFTYVNSMDPLVYFSSSPFKFYFNK 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 266 MKTILIRALDF-QTPQMCAPNDKVATYQVTRGLASLNSCVDPLLYLAGDTFRRLSR 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 LKICSLKPKQGHSKTORPEEMPISNL 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 327 ATRKSSRSEP--NVQSKSEMTLNL 351

```

```

RESULT 6
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4

```

```

Query Match          19.6% Score 362.5; DB 2; Length 373;
Best Local Similarity 27.5% Pred No. 7.9e-24;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

```

```

QY 18 MPPLIIVAVLGAINGVALGCGFCFHKMTKPSVYLFENLAVADFLIMICLPRTDYLR 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 54 LPVYILVFTIGFGLGNSVAIIMFVFMHMPGSIYVFNALADFLYVLPALFYFN 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 RRHAFDIPCRVGLFTLMMNRAGSIVFLVVAADRFKVVPHHNAVNTSTVNAAGIYC 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 KIDWIFGDWCKLQRFIFHNLYGSLFLTCISAHRYSGVYPLKSGRLKKNAYISV 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 138 TLMALVILGTYYLLLEHNLQVET-AVSC-----ESFIMESANGMHDIFQLEFYM 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 LVMALVAVGISPILFYSIGTGIRKNTITCYDTISDELYRSFYFN-----CTTVAMFCV 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 PLGILFCSEFKIWSLRRQOLARQARMKATRFIMVAIVFTCYLP-----SVSAR 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 229 PLVILIGCGYILVAKALYK-DLDSNPLRRKSTVILVLFVAVSYLPHVMTMLRAR 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 LYLMTVPSSACDPVHGALHTLSFTYVNSMDPLVYFSSSPFKFYFNKLTICSLKR 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 288 LDF-QTPQMCAPNDKVATYQVTRGLASLNSCVDPLLYLAGDTFRRLSR----- 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 QPCHSKTORPEEMPISNLGRRSCISVANSFQSD 335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 338 --ATRKSSRSEANLQSKSEDMTLNLISFKQND 370

```

```

RESULT 7
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707

```



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-44

```

```

Query Match      18.1%; Score 336; DB 1; Length 339;
Best Local Similarity 30.5%; Pred. No. 1.4e-21;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

```

```

QY 7 CRLEDITISQVMPPLLIIVAFVGLGNGVALGCFCEHMKTKWPSYVLFNLAVADFLMI 66
DB 23 CGEPTLENNLAFSFLYLDLILAVGNLALMLFIDHKSQTPANFVLMHLAVADSLCVL 82
QY 67 CLPRTDYILRRHWAAGDIPCVGLFTLANRAGSIVFLTVVADRYEKVVHPHNAVNT 126
DB 83 VLPRLVYHFGSNHMPFGEIACRLTGFLFLNMYASIVELTCSADRFALVHP--VKS 139
QY 127 ISTR--VAAGIVCT-LMALVITGVYLLLENHLCVQETAVSCSEFIMESANGHDIIMPQL 183
DB 140 LKLRPLVAHLACAFVLMVVAAMAPLVSPQTVNTNTVCLQLYRKASHHALLSLAV 199
QY 184 EFMPLGLITLFCSEKIVWSLRRQOLARQARK-KATREIMVAIVFTCYLP-SVSARL 241
DB 200 AFTEPFTVTVCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAFVLCVPHVNSV 257
QY 242 YFL-NTVPSSACDPVHGAL--HTLSFTYMSMDPLVYFSSSPFKFYKKLKISLK 298
DB 258 YVLHTRSHGASCATQRIILANRITSLTSLNGALDPIWFFVAEKFRHALCNL-LCGKR 316
QY 299 PKPGHKTQRPPEMPIS 316
DB 317 LKGPPESECKTNESLS 334

```

```

RESULT 10
US-08-812-871-3
Sequence 3, Application US/08812871
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong, Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```

```

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 992700
US-08-812-871-3

```

```

Query Match      18.1%; Score 336; DB 2; Length 339;
Best Local Similarity 30.5%; Pred. No. 1.4e-21;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

```

```

QY 7 CRLEDITISQVMPPLLIIVAFVGLGNGVALGCFCEHMKTKWPSYVLFNLAVADFLMI 66
DB 23 CGEPTLENNLAFSFLYLDLILAVGNLALMLFIDHKSQTPANFVLMHLAVADSLCVL 82
QY 67 CLPRTDYILRRHWAAGDIPCVGLFTLANRAGSIVFLTVVADRYEKVVHPHNAVNT 126
DB 83 VLPRLVYHFGSNHMPFGEIACRLTGFLFLNMYASIVELTCSADRFALVHP--VKS 139
QY 127 ISTR--VAAGIVCT-LMALVITGVYLLLENHLCVQETAVSCSEFIMESANGHDIIMPQL 183
DB 140 LKLRPLVAHLACAFVLMVVAAMAPLVSPQTVNTNTVCLQLYRKASHHALLSLAV 199
QY 184 EFMPLGLITLFCSEKIVWSLRRQOLARQARK-KATREIMVAIVFTCYLP-SVSARL 241
DB 200 AFTEPFTVTVCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAFVLCVPHVNSV 257
QY 242 YFL-NTVPSSACDPVHGAL--HTLSFTYMSMDPLVYFSSSPFKFYKKLKISLK 298
DB 258 YVLHTRSHGASCATQRIILANRITSLTSLNGALDPIWFFVAEKFRHALCNL-LCGKR 316
QY 299 PKPGHKTQRPPEMPIS 316
DB 317 LKGPPESECKTNESLS 334

```

```

RESULT 11
US-09-299-843A-44
Sequence 44, Application US/09299843A
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

```

```

1 ZIP: 60606
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: Patentin Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/09/299,843A
16
17 FILING DATE:
18
19 CLASSIFICATION: 435
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: US 09/088,337
24
25 FILING DATE: 01-JUN-1998
26
27 PRIOR APPLICATION DATA:
28
29 APPLICATION NUMBER: US 08/153,848
30
31 FILING DATE: 17-NOV-1993
32
33 PRIOR APPLICATION DATA:
34
35 APPLICATION NUMBER: US 07/977,452
36
37 FILING DATE: 17-NOV-1992
38
39 ATTORNEY/AGENT INFORMATION:
40
41 NAME: JILL E. Uhl
42
43 REGISTRATION NUMBER: 43,213
44
45 REFERENCE/DOCKET NUMBER: 27866/32059B
46
47 TELECOMMUNICATION INFORMATION:
48
49 TELEPHONE: (312) 474-6300
50
51 TELEFAX: (312) 474-0448
52
53 TELEX:
54
55 INFORMATION FOR SEQ ID NO: 44:
56
57 SEQUENCE CHARACTERISTICS:
58
59 LENGTH: 339 amino acids
60
61 TYPE: amino acid
62
63 TOPOLOGY: linear
64
65 MOLECULE TYPE: protein
66
67 US-09-299-843A-44

```

```

Query Match Similarity      18.1%; Score 336; DB 3; Length 339;
Best Local Similarity      30.5%; Pred. No. 1.4e-21;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps
9

OY      7 CRIEDTISQVAPRLIYAFVILGALGVNLGCGCFEHNKTKPSTVYLENLAVDELMI 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      23 CGQETPRLNNMLFASFYLLDFELTALVGNLTALWLFTRDKSGTPRANVFLLMHLVADLS 82
OY      67 CLPRTDYVLLRRRHHAFGIPPCRVGLFTLNNRAGSIVPLLYVANDRYKKVYHNHNAVMT 126
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      83 VLPRLVYHFGSNHMPFGELACRLTGFLELYLNNYASTYPLTCTISADRETAIVHP--VKS 139
OY      127 ISTR--VVAGYCT-LMAVLVILGTYVLLLENNLTCVOETAVSCSEFIMESAGNHDIMPOL 183
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      140 LKLRRLVLAHLACAFLMVYVAAMAPLAVSPQTQVGNHNYVGCGLYREKASHNALVSLAV 199
OY      184 EEFMLGLITLFSFKIWSLRRRQDLARARK-KATRIYVVAIVYFTICYL-P-SVASRL 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      200 APTFFPITTVTYLLIRSL--RQGRVREKRKTAAVRAIYLAFLVLCFVYHNREAV 257
OY      242 YFL-RTVPSACDPVSHGL--HTLSPFYNNMSMLDPLVYEFSSPSFKEYNKLCTCSLK 298
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      258 YVLHRSRHSASATQRIILANRITISCLTSLNGALDPIIMFYVAEKFRALCNL-LGKR 316
OY      299 PKPGHSKTQRPPEMPIS 316
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      317 LKPPPSFEKGKTESLS 334

RESULT 12
US-09-086-337B-44
; Sequence 44, Application US/09086337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schmelkart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
;

```

NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/088,337B
 FILING DATE: 01-Jun-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/153,848
 FILING DATE: 17-NOV-1993
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 634857and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:
 US-09-088-337B-44

[illegible]

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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-44

Query Match
Best Local Similarity 30.5%; Score 336; DB 5; Length 339;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

QY 7 CRIEGDTISQVMPPELLIVAFVLAGALNGVALCGFCFHKTKWPKSTVYLFENLAVADEFLMI 66
DB 23 CGQETPLENMLFASFYLLDFILALVGNLTLMLFIRDKSGTPANVFLMHLAVADLSCVL 82
QY 67 CLPFRIDYLLRRRMAFGDIPCRVGLFTLAMNRAGSIVFLTVVAAADRYEKVYHPHNAVNT 126
DB 83 VLPFRIVYHFGSNHWPFGICRLTGFLFLYLMVYASIVFLTCISADRFIAIVHP---VKS 139
QY 127 ISTR--VAAGIVCT-IMALVILGTVYLLLENHLVQETAVSCSFIMESANGMHDIMFOL 183
DB 140 LKLRRLPIAHNLACFLMVVAVAMAPLVSPTVOTNHTVVCQLYRKASHHALVSLAV 199
QY 184 EFMPLGILLFCSEFKIWSLRRQOLARQARK-KATRFIMVAIVFTICYLP-SVSARL 241
DB 200 AFTPEFTVTVCYLLIRSL--RQGLRVEKRLTKAVAMIAIVLAIFLVCVPYHVNRSV 257
QY 242 YFL-WTVPSACDPVHGAL--HTLSTYMNMSMDPLVYFESSPFKFNKLKISLK 298
DB 258 YVLYHRSHGASCATORIALANRITSCLTSLNGALDPIYEFVAEKFHALCNL-LGGR 316
QY 299 PKPGHSTKTOPREEMPTIS 316
DB 317 LKGPSPSECKTNESSLS 334

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GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: COCAVNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBER69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESS: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MOLLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07180-2

Query Match
Best Local Similarity 30.5%; Score 336; DB 5; Length 339;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

QY 7 CRIEGDTISQVMPPELLIVAFVLAGALNGVALCGFCFHKTKWPKSTVYLFENLAVADEFLMI 66
DB 23 CGQETPLENMLFASFYLLDFILALVGNLTLMLFIRDKSGTPANVFLMHLAVADLSCVL 82
QY 67 CLPFRIDYLLRRRMAFGDIPCRVGLFTLAMNRAGSIVFLTVVAAADRYEKVYHPHNAVNT 126
DB 83 VLPFRIVYHFGSNHWPFGICRLTGFLFLYLMVYASIVFLTCISADRFIAIVHP---VKS 139
QY 127 ISTR--VAAGIVCT-IMALVILGTVYLLLENHLVQETAVSCSFIMESANGMHDIMFOL 183
DB 140 LKLRRLPIAHNLACFLMVVAVAMAPLVSPTVOTNHTVVCQLYRKASHHALVSLAV 199
QY 184 EFMPLGILLFCSEFKIWSLRRQOLARQARK-KATRFIMVAIVFTICYLP-SVSARL 241
DB 200 AFTPEFTVTVCYLLIRSL--RQGLRVEKRLTKAVAMIAIVLAIFLVCVPYHVNRSV 257
QY 242 YFL-WTVPSACDPVHGAL--HTLSTYMNMSMDPLVYFESSPFKFNKLKISLK 298
DB 258 YVLYHRSHGASCATORIALANRITSCLTSLNGALDPIYEFVAEKFHALCNL-LGGR 316
QY 299 PKPGHSTKTOPREEMPTIS 316
DB 317 LKGPSPSECKTNESSLS 334

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RESULT 14
 PCT-US95-07180-2
 : Sequence 2, Application PC/TUS9507180

RESULT 15
 US-08-467-948A-30
 : Sequence 30, Application US/08467948A
 : Patent No. 5998164
 : GENERAL INFORMATION:
 : APPLICANT: LI, YI

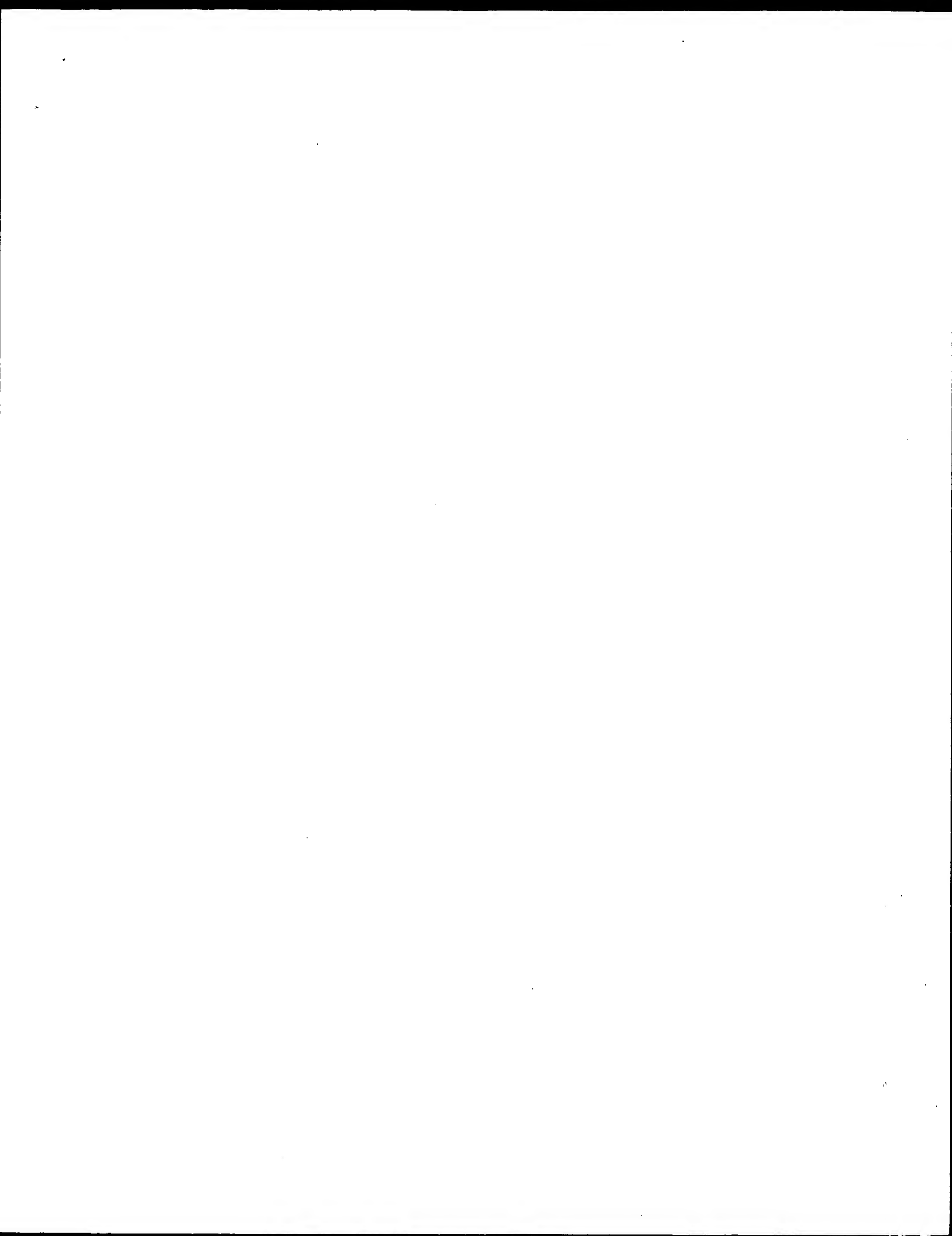
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1  APPLICANT: CAO, LIANG
2  APPLICANT: NI, JIAN
3  APPLICANT: GENTZ, REINER
4  APPLICANT: BULT, CAROL J.
5  APPLICANT: SUTTON II, GRANGER G.
6  APPLICANT: ROSEN, CRAIG A.
7  TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
8  TITLE OF INVENTION: Coupled Receptor GPR2
9  NUMBER OF SEQUENCES: 30
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
12 STREET: 1100 NEW YORK AVE., NW, SUITE 600
13 CITY: WASHINGTON
14 STATE: DC
15 COUNTRY: USA
16 ZIP: 20005
17
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: FLOPPY DISK
20 COMPUTER: IBM PC COMPATIBLE
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
23
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/467,948A
26 FILING DATE: 06-JUN-1995
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: PCT/US95/04079
30 FILING DATE: 30-MAR-1995
31 ATTORNEY/AGENT INFORMATION:
32 NAME: STEFFE, ERIC K.
33 REGISTRATION NUMBER: 36,688
34 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 202-371-2600
37 TELEFAX: 202-371-2540
38 INFORMATION FOR SEQ ID NO: 30:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 302 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: single
43 TOPOLOGY: not relevant
44 MOLECULE TYPE: peptide
45
46 US-08-467-948A-30

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[illegible]

Search completed: March 26, 2003, 19:39:49
Job time : 31 secs



GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:38:54 ; Search time 34 Seconds
(without alignments)
597.600 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853

Sequence: 1 MYNSCCRIEPTISQVMP.....ANSFQSQDQMDPIHEWH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1853	100.0	346	10	US-09-862-274-2
2	1853	100.0	346	10	US-09-942-374-2
3	1849	99.8	346	9	US-10-094-417-8
4	1739	93.8	342	9	US-10-092-135-2
5	880.5	47.5	387	9	US-10-092-135-8
6	880.5	47.5	387	10	US-09-944-807-21
7	529	28.5	423	10	US-09-826-508-40
8	448.5	24.2	319	9	US-10-092-135-9
9	446.5	24.1	319	9	US-10-109-549-2
10	366.5	19.8	330	10	US-09-826-791-2
11	366.5	19.8	346	9	US-09-828-478-2
12	366.5	19.8	346	10	US-09-826-791-6
13	366.5	19.8	346	10	US-09-866-230-7
14	366.5	19.8	346	10	US-09-866-230-9
15	364	19.6	362	9	US-10-092-135-3
16	364	19.6	362	9	US-10-092-135-4
17	362.5	19.6	373	9	US-10-092-135-5
18	358.5	19.3	373	9	US-10-092-135-7
19	354	19.1	373	9	US-10-092-135-6

20	343	18.5	299	9	US-10-270-144-4	Sequence 4, Appli
21	336	18.1	339	9	US-09-828-478-4	Sequence 4, Appli
22	336	18.1	339	10	US-09-848-989-12	Sequence 12, Appli
23	336	18.1	339	10	US-09-788-133-2	Sequence 2, Appli
24	336	18.1	367	9	US-09-828-478-6	Sequence 6, Appli
25	328.5	17.7	302	9	US-10-024-494-30	Sequence 30, Appli
26	327	17.6	309	10	US-09-768-877-20	Sequence 20, Appli
27	325	17.5	344	9	US-10-024-494-8	Sequence 8, Appli
28	320	17.3	341	9	US-10-270-587-3	Sequence 3, Appli
29	318	17.2	253	9	US-10-116-232-10	Sequence 10, Appli
30	309.5	16.7	363	9	US-09-992-331-14	Sequence 14, Appli
31	305.5	16.5	391	9	US-09-990-940-20	Sequence 20, Appli
32	305	16.5	337	9	US-09-828-478-5	Sequence 5, Appli
33	305	16.5	337	10	US-09-866-230-8	Sequence 8, Appli
34	305	16.5	372	9	US-10-167-192-5	Sequence 5, Appli
35	305	16.5	372	10	US-09-768-894A-2	Sequence 2, Appli
36	302	16.3	337	9	US-10-167-192-3	Sequence 3, Appli
37	302	16.3	391	12	US-09-966-871-82	Sequence 82, Appli
38	302	16.3	391	12	US-10-039-645-82	Sequence 82, Appli
39	300.5	16.2	369	10	US-09-823-114-9	Sequence 9, Appli
40	300	16.2	428	9	US-09-992-331-15	Sequence 15, Appli
41	298.5	16.1	418	9	US-09-992-331-17	Sequence 17, Appli
42	298	16.1	428	9	US-09-992-331-16	Sequence 16, Appli
43	294	15.9	372	9	US-10-112-599A-4	Sequence 4, Appli
44	293	15.8	362	9	US-09-992-331-13	Sequence 13, Appli
45	292.5	15.8	365	9	US-10-109-533A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-862-274-2
Sequence 2, Application US/09862274
Patent No. US20020052022A1
GENERAL INFORMATION:
APPLICANT: ELSHOURBAGY, NABIL
APPLICANT: SHABON, USMAN
APPLICANT: SHABON, USMAN
APPLICANT: IGAR, DIANE MICHELE
TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE
FILE REFERENCE: GP-70703-1
CURRENT APPLICATION NUMBER: US/09/862,274
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 09/580,675
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: GB 0026839.1
PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-862-274-2

Query Match 100.0% Score 1853; DB 10; Length 346;
Best Local Similarity 100.0% Pred. No. 1.6e-169;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MYNSCCRIEPTISQVMPPLIYAFVIGALGNGVALGFCFHHKTKPKSTVYLFNLAVA 60
QY DELMITCLPEFTDYLLRRRHHAFGDI PCRVGLFTLANRAGSIYELTVVADRFXKVVHP 120
DB DELMITCLPEFTDYLLRRRHHAFGDI PCRVGLFTLANRAGSIYELTVVADRFXKVVHP 120
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DB 121 HHAVTISTRAAAGIVCTLMALVYIIGTYLLLENHLCYQETFAVCESTFMSANGMDIM 180

QY 181 FOLEFMPGLIIFCSFKIWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 DB 181 FOLEFMPGLIIFCSFKIWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
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 DB 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKIKISLKP 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346

RESULT 2
 US-09-942-374-2
 ; Sequence 2, Application US/09942374
 ; Patent No. US20020137063A1

GENERAL INFORMATION:
 APPLICANT: Glucksmann, Maria Alexandra
 APPLICANT: Gimeno, Ruth
 TITLE OF INVENTION: 57242, a Human G-Protein Coupled
 TITLE OF INVENTION: Receptor Family Member and Uses Therefor
 FILE REFERENCE: MP12000-368P1R
 CURRENT APPLICATION NUMBER: US/09/942,374
 CURRENT FILING DATE: 2001-08-29
 PRIOR APPLICATION NUMBER: US 60/228,409
 PRIOR FILING DATE: 2000-08-29
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 346
 TYPE: PRT
 ORGANISM: human
 US-09-942-374-2

Query Match 100.0%; Score 1853; DB 10; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-169;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLLIYAFVLGALGNGVALCGFCFHMKTWKPSTYVLENLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLLIYAFVLGALGNGVALCGFCFHMKTWKPSTYVLENLAVA 60
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 DB 61 DELLMLICLPFRDYLLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 QY 121 HHAVENTISTRVAAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 DB 121 HHAVENTISTRVAAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 QY 181 FOLEFMPGLIIFCSFKIWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 DB 181 FOLEFMPGLIIFCSFKIWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKIKISLKP 300
 DB 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKIKISLKP 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346

RESULT 3
 US-10-094-417-8
 ; Sequence 8, Application US/10094417
 ; Publication No. US20030045685A1
 ; GENERAL INFORMATION:
 APPLICANT: Tian, Hui
 APPLICANT: Zhao, Jiayang
 APPLICANT: Chen, Jin-long

APPLICANT: Cutler, Gene
 APPLICANT: Tularik Inc.
 TITLE OF INVENTION: No. US20030045685A1el Receptors
 FILE REFERENCE: 018781-008110US
 CURRENT APPLICATION NUMBER: US/10/094,417
 CURRENT FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: US 09/802,803
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: US 60/276,649
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 8
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR183
 US-10-094-417-8

Query Match 99.8%; Score 1849; DB 9; Length 346;
 Best Local Similarity 99.7%; Pred. No. 3.9e-169;
 Matches 345; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 61 DELLMLICLPFRDYLLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 DB 61 DELLMLICLPFRDYLLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 QY 121 HHAVENTISTRVAAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 DB 121 HHAVENTISTRVAAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 QY 181 FOLEFMPGLIIFCSFKIWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 DB 181 FOLEFMPGLIIFCSFKIWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKIKISLKP 300
 DB 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKIKISLKP 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSQSDGQMDPHIVEWH 346

RESULT 4
 US-10-092-135-2
 ; Sequence 2, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
 FILE REFERENCE: D0134.NP
 CURRENT APPLICATION NUMBER: US/10/092,135
 CURRENT FILING DATE: 2002-03-06
 PRIOR APPLICATION NUMBER: US 60/273,808
 PRIOR FILING DATE: 2001-03-07
 PRIOR APPLICATION NUMBER: US 60/278,983
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: PatentIn Version 3.0
 SEQ ID NO 2
 LENGTH: 342
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-092-135-2

Query Match 93.8%; Score 1739; DB 9; Length 342;

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Db 316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPPSP 355

RESULT 6
US-09-944-807-21

Patent No. US20020119494A1
GENERAL INFORMATION:

TITLE OF INVENTION: Method for identifying substances which positively influence inflammatory conditions of chronic

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; FILE REFERENCE: 082_00n
; CURRENT APPLICATION NUMBER: US/09/944,807

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; PRIOR APPLICATION NUMBER: UK 0021484.1
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; PRIOR FILING DATE: 2000-09-01

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;; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 21
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; TYPE: PRT
; ORGANISM: Homo sapiens

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Query Match	Score	DB 10;	Length
47.5%	880.5;	387;	

Matches	1/8; Conservative	49;	Mismatches	107,	Indels	7;	Gaps	4
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20Y INDCMIAIILDCEDMOIYVLYHEDNNNDLIGNCFRANVCISFSLCHIFEMWDAWFLE 13

Db 197 FLLPGLLFCSSARIWLSLRQ-QMDRAKIKRAITFLINVAIVEICFLPSSVVRIRIF 25

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QY 300 KQPGHKTÖRPEEMPISNLGRSCISVANSFQSQSDQWDP 340
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US-09-826-508-40
: Sequence 40, Application US/09826508

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; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy

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1 TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
2
3 TITLE OF INVENTION: and Polynucleotides
4
5 FIRST INVENTORS: OR 10744000

: CURRENT APPLICATION NUMBER: US/09/826,508
 : CURRENT FILING DATE: 2001-04-05
 : NUMBER OF SEQ ID NOS: 40

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40

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; LENGTH: 423
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-508-40

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Query Match	28.5%;	Score 529;	DB 10;	Length 423;
Best Local Similarity	39.2%;	Pred. No. 1.1e-42;		
Matches 115;	Conservative 48;	Mismatches 108;	Indels 22;	Gaps 7

QY	4	GSCRCIEGDTISOVMPLIIVAFVGLMGLNGVNLGCSCFEMKIKRSHVIVLEINLAVDFL	63
Db	81	GPCHPSTSSLSASAPLIPALILEEVLGLVGNLSLAEFICHTIRPMWSNVEFLVSIYAADF	140
QY	64	LMICLFEPRDIYLLRRRHHAFEDICRGLFTLLMNRGSLVETLVYAADRYKVVHNNHA	122
Db	141	LISNLEPLRDVYDILHEHTRFCAACKVYLLNLSLSTNRASVAFETALALMKYLRKVPHV	200
QY	124	VNFISTRVAGVICTMLAVLLIGTVYVLELHNCVOE-TAVSCSEPIM---ESANGMHD	178
Db	201	LSRASVGAARAVAGGLWGI-----LLNGHLLSTFSSPSOLSRVGTRKPSASLRHQ	256
QY	179	IMQLEFPMPGLIIIFGSEKIVWSLRRROOLAROARKKATREINVAIVPTCYLPSV-	237
Db	255	AKLIEEFPPLALILFAIVISGLTIRNR-GIGGAGAGFORAMRYLAVVAVYICLPSII	313
QY	238	--SARLYELMTVPSSA--COPVGHALHITSTIYWNKSLDPIVYSSPSF	285
Db	314	FGASVAVWVWISACRSIDLCTQLERHG-----SLATITNSVLDVLEICRSSPWF	362

[illegible]

```
QY      241 --LYELWIVPSSACDPBVHGALHTLSTFYMNMSMLDPLVYYFSSPSPEKRYNKL 292
       ::   : |   : | | | : : : | | | | | A | : :
Db      243 VLMHIFQNIGSCRALCAVAHTSDVYGLTLYLHVSVPNVVCYCFSSPTFSSSYRVR 296
```

```

RESULT 9
US-10-109-549-2
; Sequence 2, Application US/10109549
; Patent No. US20020170081A1
; GENERAL INFORMATION:
; APPLICANT: Brennan, Thomas J.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GPR31 GENE
; TITLE OF INVENTION: DISRUPTIONS
; FILE REFERENCE: R-180
; CURRENT APPLICATION NUMBER: US/10/109,549
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/280,512
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/326,669
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PR1
; ORGANISM: Mus musculus
US-10-109-549-2

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[illegible]

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; PATENT NO US20020150901A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Murphy, Andrew, et al.

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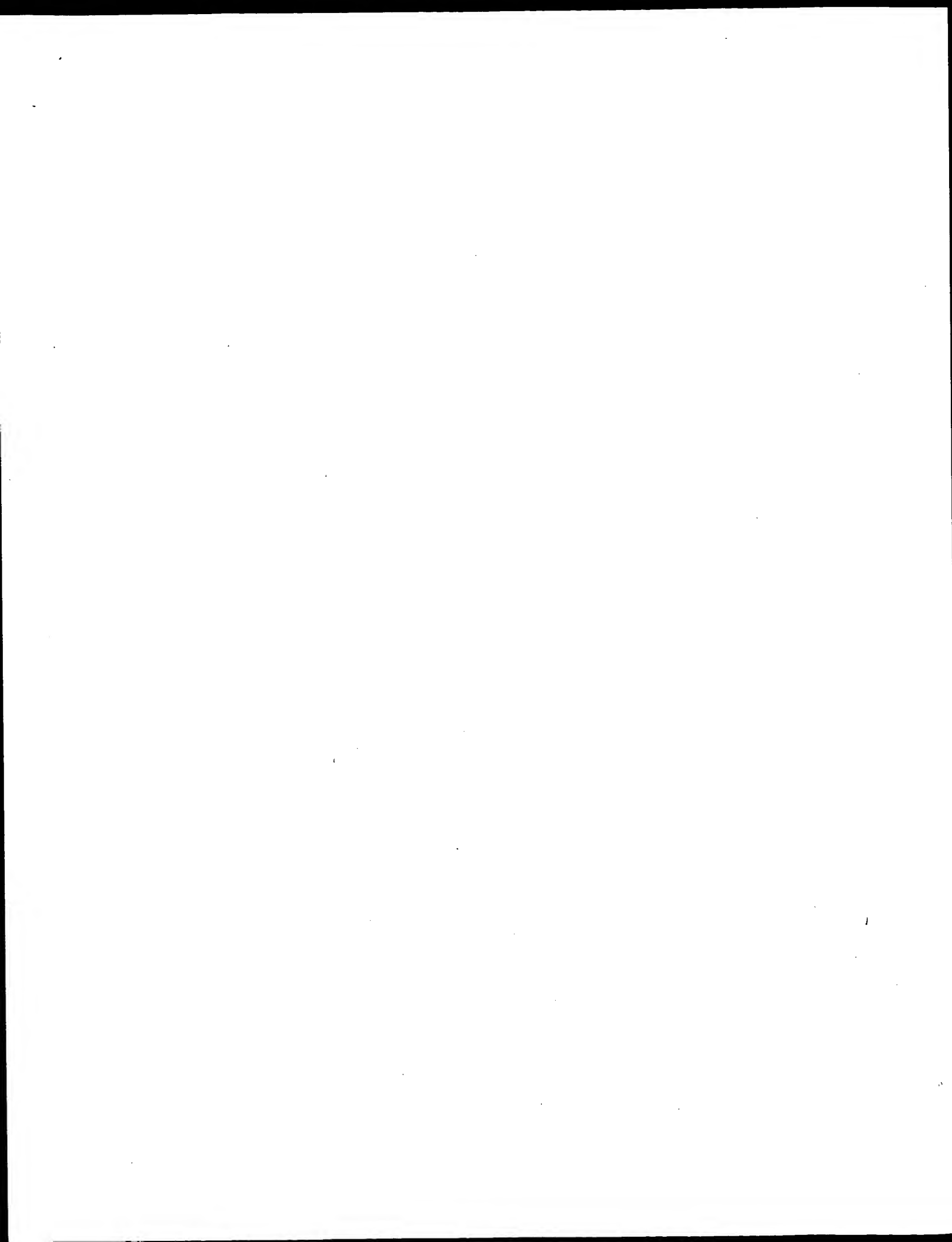
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: TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Man
: FILE REFERENCE: REG 771A
: CURRENT APPLICATION NUMBER: US/09/866,230
: CURRENT FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/207,725
: PRIOR FILING DATE: 2000-05-26
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 7
: LENGTH: 346
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-866-230-7

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Thu Mar 27 09:01:05 2003

us-09-942-374-2.rapb



GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 19:35:54 ; Search time 20 Seconds

(without alignments)
1663.126 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853
Sequence: 1 MYNSGCCRIEDDTISQVMPANSFGSOSDGGMDPHIYEMH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : PIR_73:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	880.5	47.5	387	2	169202
2	364	19.6	362	2	S33733
3	362.5	19.6	373	2	JC4162
4	354	19.1	373	2	JC4737
5	343.5	18.5	370	2	JC5549
6	339	18.3	308	2	I50241
7	324	17.5	344	2	T09508
8	320	17.3	373	2	A47556
9	310.5	16.8	420	2	I51667
10	309.5	16.7	363	2	I57940
11	307	16.6	391	2	C41795
12	305.5	16.5	391	2	A41795
13	305.5	16.5	359	2	A39297
14	304.5	16.4	359	2	S15403
15	302.5	16.3	369	2	B41795
16	302	16.3	364	2	J01488
17	302	16.3	399	2	I48705
18	300.5	16.2	369	2	A45291
19	300.5	16.2	369	2	D41795
20	300	16.2	328	2	I55450
21	300	16.2	384	2	A47249
22	300	16.2	428	2	A44021
23	299.5	16.2	369	2	JC2083
24	299	16.1	388	2	JN0605
25	298.5	16.1	418	2	A46226
26	298.5	16.1	428	2	A43448
27	298	16.1	428	2	S30508
28	297	16.0	397	2	S66518
29	296.5	16.0	346	2	S29248

30	296	16.0	359	2	A48857	angiotensin II rec
31	296	16.0	375	2	A54946	P-20-nucleotide re
32	295	15.9	384	2	JC4629	somatostatin recep
33	294	15.9	372	2	I38532	delta opioid recep
34	292.5	15.8	361	2	JC5653	G protein-coupled
35	292	15.8	359	2	JC5498	G protein-coupled
36	291.5	15.7	359	2	JC4425	angiotensin II rec
37	291.5	15.7	359	2	JC2134	angiotensin II rec
38	290	15.7	372	2	S34592	delta opioid recep
39	289	15.6	359	2	JC1104	angiotensin II rec
40	288	15.5	355	2	A45177	chemokine (G-C) re
41	288	15.5	372	2	B48227	delta opioid recep
42	287.5	15.5	365	2	S68208	G protein-coupled
43	287.5	15.5	371	2	JC5796	probable chemokine
44	286.5	15.5	359	2	JH0621	angiotensin II rec
45	286.5	15.5	423	2	JC7677	allatostatin recep

ALIGNMENTS

RESULT 1

169202 G protein-coupled receptor HM74 - human

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 19-May-2000

C:Accession: I69202

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte

A:Reference number: I54751; MUID:94092629; PMID:7505609

A:Accession: I69202

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-387 <RES>

A:Cross-references: GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867

C:Genetics:

A:Gene: HM74

C:Superfamily: G protein-coupled receptor 4

Query Match	47.5%	Score 880.5;	DB 2;	Length 387;
Best Local Similarity	52.2%;	Pred. No. 5.1e-74;		
Matches 178;	Conservative 49;	Mismatches 107;	Indels 7;	Gaps 4;
QY	5	SCCRREGDTISQVMPDLIVAFVLCALGVYALGCECFHMTKPSVYVFLNLAFADEL	64	
DB	17	NCCVFRDDFTAKVLPVPLVGLERIFGLGGLALMTFCFLHLSWSSKIFLNLAVADFL	76	
QY	65	MCLEPFRDYLRARRHMAFGDIPCRVGLFTLAMNRASTIVELVVAADRYEKVPHHVA	124	
DB	77	ICLPEFVMDYVRRSDWNGDIPCRVLVLFMFAMNROGSLIFLVVAVDYRFRVPHHAL	136	
QY	125	NTISRVAAIVCTMALVILGTVYLLBNHLCVOETAVSCSEFMESANGHDMFDE	184	
DB	137	NKISWMTAAIISCLMGLVIGLVHLKLLIQNGPANVCISFICHTFRHEAMFLE	196	
QY	185	FEMPIGLIFCFSEKIVYSRRROQLARQAMKATPIIVVATVITVQVLSARVEL	244	
DB	197	FLPLGLIIFCSARITWSLRORQMDRAKIKRALTFTVVAIVAVICFLSVVVRKIF	255	
QY	245	KVVPSSA--CD--PSVHGHITLSFTYVMSMDPLVYFSSPFPKYNKLKICSLKP	299	
DB	256	WLHTSGTQNCVYRSDVDAFTITLSFTYVMSMDPLVYFSSPFPKYNKLKICSLKP	315	
QY	300	KOPGHSKTORPEMPISNLGRSCISVANSFOSQSDGMDP	340	
DB	316	KMTGEPDNKRSTSVELTGDPNKT-RGADEALMANSGEPWSP	355	
RESULT 2				
S33733				
G protein-coupled receptor - chicken				
C:Species: Gallus gallus (chicken)				

Query Match	19.6%	Score 364	DB 2	Length 362
Best Local Similarity	29.1%	Pred. No. 4,66-26		
Matches	95	Conservative 58	Mismatches 130	Indels 44
				Gaps 7
QY	18	MPPLLVAFLVGLALGNGVALCGFCFHNMTWKRPSVYLFFNLAVADELMLICLPERTDYLR	77	
Db	43	LPFVYLIVFTGTLGSAVAIMFVEHMRPMWSISVYMENLALDELVLPLPLITYYR	102	
QY	78	RHRMGAGDIPCRGGLFTLAMNAGSIVELYVAADRIFFKVYVHPHNAVNTISTVAAIGVC	137	
Db	103	KTDWIFGDMWCKLQRFIFHNLYGSLFLPFCISVHRYGVNPLKSLGRKKNAVYSS	162	
QY	138	TLMAVL-----GTVLELLLNHCVOETA-----VGESESTMSANGMD	178	
Db	163	LVAALVAVAVIAPLFTSGIVGRNRKTTTCYTDTTADVELRYSTFYVSMCTTVE-----	214	
QY	179	IMQLEFEMPLGIIILFCSEFKIWSLRRRQOLBARAKMKATRFMVAVAYETCYLP--	235	
Db	215	-----FCAPFVILIGCVLIYKALIKR-DLDNSPLKRKSLYLIYLIYFANVSLYFPFV	267	
QY	236	-----SVSADLYFLMTVPSSACDPVHGALHTLSFTYNSMDLPVLYESSPSFPAFYK	291	
Db	268	MKTLNLRALDF-QIPQMCAPFNDKRYATYQYTRGLASLNSCVDPLFLYFLAGDFFRRRLSR	326	
QY	292	LKTCSLAKPKQPGHSTQREEMPISNL	318	
Db	327	AIKRSRSRSE--NWQSKSEENTLNL	351	

Best Local Similarity 27.5%; Pred. No.6,6e-26;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

```
OY      18 MPRLLVAVPLGLGNGVALCGCFHMKTKWSTVYLLENLAADFLIMCLPRTDYLR   77  
          : : : : : | | | | | : | | | | | : | | | | | : | |  
DB       54 LRPVLYLVLITIGLGNSVAIWMFVFHKRPMWSGISGYVMFIADLFYLTLPALITYFN  113  
OY       78 RRRMAATDIPCRGGLETLTLMNRAGSIVFLTVNAADEPFVPHHHANNINISPVANGYC  137  
          : | | | | | : : : | : | | | | | : | | | | | : | |  
DB      114 KIDMIFGDAMKIQRIPIFYNNLXGSTILFLPICIAHRISGVYPPLSKGRKKNNAYISV  173  
OY     138 TLMALVILTCTYLLLENHLVOET-AVSC-----ESFTIESANGMHDIWFQLEFP    187  
          : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB     174 LWLIYVVISPILTFYSGTGIIRKNKTICTCYDTSDIELSYFIYSN-----CITVMEFCV  228  
OY     188 PLGITLFGCFKIYWLSLRROQLARQRMRKAIRFIWVAIVPTCYLP-----SVSR    240  
          || : ||| : | | | | | : : : : | : : : | : | : | : | : |  
DB     229 PVLIIICGCGLIVRALITY-LDINSPLRKRSIYLYIVTVFAVSVIPHYAKTMELRAR    287  
OY     241 LVFLMTVPSSACDPNVHGALHTLSEFTYNNMSMLDLPLYVFSSEPFRFKYCSLKPK    300  
DB     288 LDFF-QPEMGCAENDRVYAYVTYTRGLASLNSCDPILTYLDADTFPRRLSR-----  337  
OY     301 QPGHSKTOPHEEMPISNLGRRCISVANSPQSOD 335  
DB     338 --ATRKRARRSEANLOSKSEDMDTNLTISEFKONGD 370
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RESULT 4
JC4737

G protein-coupled receptor p2y1 - human

N.Alternate names: p2y1 purinergic receptor; p2y1 purinoceptor
C.Species: Homo sapiens (man)
C.Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 17-Nov-2000
C.Accession: JC4737; Jc4615; S54253

R.Janssens, R.; Commun, D.; Piotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A.Title: Cloning and tissue distribution of the human p2y1 receptor.

A.Reference number: JC4737; PMID:96205320; PMID:8630005

A:Molecule type: DNA

A:Residues: 1-373 <JAN>

A:Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439

R.Ayanathan, K.; webbs, T.E.; Sandhu, A.K.; Altwal, R.S.; Barnard, E.A.; Kunapuli, S
Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A>Title: Cloning and chromosomal localization of the human p2y1 purinoceptor.

A.Reference number: JC4615; MUID:96158962; PMID:8579591

A:Accession: JC4615

A:Molecule type: mRNA

A:Residues: 1-373 <AYI>

A:Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

A:Experimental source: eythro leukemia cells
R.leon, C.; Val, C.; Cazeneuve, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995

A>Description: Cloning of a human putative p2y receptor.

A:Reference number: S54253

A:Accession: S54253

A>Status: preliminary

A:Molecule type: mRNA

F:52-77/Domain: transmembrane #status predicted <TM>
E:52-77/Domain: transmembrane #status predicted <TM>
F:88-111/Domain: transmembrane #status predicted <TM>
F:124-152/Domain: transmembrane #status predicted <TM>
F:171-191/Domain: transmembrane #status predicted <TM>
F:214-237/Domain: transmembrane #status predicted <TM>

C.Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
A:Map position: 3pter-3qter
A:Superfamily: Arp receptor p2u

C.Comment: This receptor belongs to a family of G protein-coupled receptors. It respo
C.Genetics:

A:Gene: p2y1; GDB:p2RY1

A:Cross-references: GDB:677125; OMIM:601167

A:Reference number: 157940; MUID:93125499; PMID:1362243
 A:Accession: 157940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-363 <OCAL>
 A:Cross-references: GB:L04535; NID:9409238; PIDN:AA17029.1; PID:9409239
 R.O'Carroll, A.M.; Lohait, S.J.; Konig, M.; Mahan, L.C.
 Mol. Pharmacol. 44, 1278, 1993
 A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
 A:Reference number: 157949; MUID:94088493; PMID:8264565
 A:Accession: 157949
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 341-363 <OCA2>
 A:Cross-references: GB:s67370; NID:9455947; PIDN:AA29371.1; PID:9455948
 A:Experimental source: pituitary
 R.Peneta, R.; Greenwood, M.; Patel, Y.C.
 submitted to the EMBL Data Library, August 1993
 A:Description: Correction of the nucleotide and amino acid sequence of the rat somatosta
 A:Reference number: S39244
 A:Accession: S39244
 A:Molecule type: mRNA
 A:Residues: 309-363 <PEN>
 A:Cross-references: EMBL:X74828; NID:9433911; PIDN:CAA52825.1; PID:9433912
 C:Genetics:
 A:Gene: SSTR5
 C:Superfamily: vertebrate rhodopsin

Query Match 16.7%; Score 309.5; DB 2; Length 363;
 Best Local Similarity 29.6%; Pred. No. 5,4e-21;
 Matches 96; Conservative 53; Mismatches 148; Indels 27; Gaps 9;

QY 17 VMPPLIVFVIGALGNGVLCGFCFHMKTWKPSTVYLEFNLADELMLICPFRDYL 76
 Db 39 LPEVLLCTVGLSGNTLIVYVLRHAAKMTVTNYILNLAVADLEMLGPGTATONA 98
 QY 77 RRRHNAFGDIPCRVGLFTLANNRAGSIVLTVAAADRFKVVHPHNAVITSTRVAGIV 136
 Db 99 VVSYPWFSGFLCRVLTVDGINFTIFCLAMVSDRYLAVVHPLRSAMRRPRKAKMAS 158
 QY 137 CTLMAVLIIGTYLLLEHNLQVETAVSCSEFTMESANGMDIMQ---LEFMPGLIT 192
 Db 159 AAWWFSLMISPLLV--PADVOEGWGTCLMSPEFVGLMGAAFLIYTSVLGFFGLIYI 216
 QY 193 LQCSFIVWSLR--RQQLARQARK-KATRPIMVAIVETCYLPSASALTYL-RTV 247
 Db 217 CICYLLIVVKKRAGMRVSSRRRSEPKVTRVVVVVAVLVEGVCMPEFIVINVLATFL 276
 QY 248 PSSACDPVHGALHTLSTFYNNMSMDPLVYVYSSPSPFKFNKLKIC-----SLKP 299
 Db 277 PE---EPTASGLYFVVVLSYANSCANPLLYGLFSDNFRQSRKVLCLRRGYGMEDADA 332
 QY 300 KQPGHKTQRPPEMPLISNIGRSC 323
 Db 333 IEPRPDKSGRPQ---ATLPTRSC 352

RESULT 11

C41795
 somatostatin receptor 1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
 C:Accession: C41795
 R.Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A:Title: Cloning and functional characterization of a family of human and mouse somatost
 A:Reference number: A41795; MUID:92108031; PMID:1346068
 A:Accession: C41795
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-391 <YAM>
 A:Cross-references: GB:M81831; NID:9201058; PIDN:AAA58255.1; PID:9201059
 C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
 Query Match 16.6%; Score 307; DB 2; Length 391;
 Best Local Similarity 25.7%; Pred. No. 9.9e-21;
 Matches 85; Conservative 62; Mismatches 130; Indels 54; Gaps 9;

QY 4 GSCRIED-----TISQVMPPLILVAV-----LGAINGVALCGF 40
 Db 24 GACSGPSSGAAADMEERGNAQNGTLSEQSAIILISFYVCLVGLCGNSMVIYI 83
 QY 41 CFHMKTKPSTVYLEFNLADELMLICPFRDYLRRHNAEGDIPCRVGLFTLANNRA 100
 Db 84 LRYAKMTATNYILNLAIADDELMLISVPLVSTL-LRHMPGALLCRVLSDAVNMF 142
 QY 101 GSIYELTVAAADRFKVVHPHNAVITSTRVAGICTMAVLIIGTYLLLEHNLQV 159
 Db 143 TSICLVTVLSVDRVAVVHPHNAKRVKAVNGLVWVLSLILPLTVVSSRTAANS 202
 QY 160 FTAVSCSEFTMESANGMD---IMFOLPEFMPGLITFC-----SPKIVWSLR 204
 Db 203 DGTACNNLMPEPQRMVGLVLTFLMGLFLPVGALCLCYVLIAMRWALKAGQQR 262
 QY 205 RQQLARQARKKATRPIMVAIVETCYLPSASARLYFLMTVPSSACDPVHGALHTL 264
 Db 263 KRSE-----RKITLMVMVMVAVFVICWMPFYVQLVNVFAEQDDAT-----VSQLSV 309
 QY 265 SFTYNNMSMDPLVYVYSSPSPFKFNKLKIC 295
 Db 310 ILGYANSCANPLLYGLFSDNFRKRSFQRT-LC 339

RESULT 12

A41795
 somatostatin receptor 1 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
 C:Accession: A41795
 R.Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A:Title: Cloning and functional characterization of a family of human and mouse somat
 A:Reference number: A41795; MUID:92108031; PMID:1346068
 A:Accession: A41795
 A:Molecule type: DNA
 A:Residues: 1-391 <YAM>
 A:Cross-references: GB:M81829; NID:9307433; PIDN:AAA58247.1; PID:9307434
 A>Note: Sequence extracted from NCBI backbone (NCBIN:74767, NCBIPI:74768)
 C:Genetics:
 A:Gene: GDB:SSTR1
 A:Cross-references: GDB:134185; OMIM:182451
 A:Map position: 14q13-14q13
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein;
 F:58-84/Domain: transmembrane #status predicted <TM1>
 F:95-120/Domain: transmembrane #status predicted <TM2>
 F:132-153/Domain: transmembrane #status predicted <TM3>
 F:173-195/Domain: transmembrane #status predicted <TM4>
 F:220-250/Domain: transmembrane #status predicted <TM5>
 F:269-296/Domain: transmembrane #status predicted <TM6>
 F:302-326/Domain: transmembrane #status predicted <TM7>
 F:4,44,48,381/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:130-208/Disulfide bonds: #status predicted
 F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pre
 F:265/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre
 F:339/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 16.5%; Score 305.5; DB 2; Length 391;
 Best Local Similarity 26.3%; Pred. No. 1.4e-20;
 Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;

QY 10 EGDTSIQVMPPLILVAV-----LGAINGVALCGFCFHMKTWKPSTVYLEFNLADEL 63
 Db 47 ONGTLSEGGASAILISFYVCLVGLCGNSGMVIYILRYAKMTATNYILNLAIADDEL 106

```

OY      64 IMICLFETDYDYLRRRHMAFDIDICRVGFTLLAMNRAGSIVFTLVVAADFFVYVPRHNA 123
      || : || : || : || : || : || : || : || : || : || : || : || : || :
Db      107 IMLSPFLVYSTL-LRRHPRALLCRLLVSDAVNMMTSTYCTLTLSVDRYAVNPRICA 165
OY      124 VNTISTRVAGICTLMAVLILGTVYLLENNHCY-OETAVSCSEFTMESANGMHD--- 178
Db      166 ARYRRPTAKVVNNGVAVLSTVILLPIVTVSRTAANSDDGTVAACNMMLPEPAQFRLGFAVL 225
OY      179 IMFOLEFFMPGLILFC-----SPKIYMSLRRQOLARQAMRKATRFIVVAI 227
Db      226 YTFLMGFLTPRGALCCLCYVLIAMNRVALKAGNQKRSE-----KRTILMVMVVM 278
OY      228 VFTCYLPYSVARLYFTWYVSSACDPSVHGALHTLSTFYNNMSMLDPLVYVYSPSPFK 287
      || : || : || : || : || : || : || : || : || : || : || : || :
Db      279 VFVLCMMFFVYVQLVNFVFAEDDDAT-----VSOLSTVLGYANSCAMPILYGLSDNFKR 332
OY      288 FYNNKLKIC 295
      || : || : ||
Db      333 SFQRI-LC 339

```

RESULT 13

somatostatin receptor - rat
 N:Alternate names: probable G-protein-coupled receptor; SMF receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
 C:Accession: A39297; A45102; S20088
 R:Meerloof, W.; Paust, H.-J.; Schoenrock, C.; Richter, D.
 DNA Cell Biol. 10, 689-694, 1991
 A:Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed
 A:Reference number: A39297; MUID:92096119; PMID:1661599
 A:Accession: A39297
 A:Molecule type: mRNA
 A:Residues: 1-391 <MEY>
 A:Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; PID:g56310
 A:Experimental source: brain
 A>Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated
 R:Li, A.-J.; Forte, M.; North, R.A.; Koss, C.A.; Snyder, S.H.
 J. Biol. Chem. 267, 21307-21312, 1992
 A:Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
 A:Reference number: A45102; MUID:93016064; PMID:1400442
 A:Accession: A45102
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-391 <LI1>
 A:Experimental source: brain
 A>Note: Sequence extracted from NCBI backbone (NCBIP:116692)
 C:Subfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match	16.5%;	Score 305.5;	DB 2;	Length 391;
Best Local Similarity	26.3%;	Pred. No. 1.4e-20;		
Matches	81;	Conservative	62;	Mismatches 128;
			Indels	37;
			Gaps	8;

```

OY      10 EGDRTISQVMPPELLLYIAEVE-----LGAAGNVALVCGCFFHKKTPKPSVYLLENLAADF 63
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      47 QNGTISEGQSAILLSFTSYSVCLGVGLCGNSMYIYLLRAKMTATNIITLNALDEL 106
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      64 LMICLPERTDIYLRRRHAFEDIPCRVGLFTLAMNRASIVELTVADRYEKVVPHNA 123
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      107 LMLSPFLVTSTL-LRHHPFGALLCRLVLSDAVANMFSTICYCLTVLSVDYRAVAVHP IKA 165
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      124 VNTISTRAAGIVCTIMALVILGVYILLLEHLGV-OETANSCESEFIMESANGNH---- 178
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      166 ARTRRPYAKVNWGMVWLSLVLTPLIVSRSTAANDSGVTACMMLPEPQRWLGEVL 225
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      179 IMFOLSEPFMPGIILFC-----SFRIVMSLRRFOOLAQAAMRKATRPERINVAI 227
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      226 YTFLMGFLLPYGAICLCYVLIIAKMRYALKAGNQOKRRSE-----RKITLVMNVVM 278
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      228 VFITCIPLSVSAKLVELMTVSSACDSYGICALIITLTSFYTMNSMDPLVIYYSSSEFPK 287

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```

Db      279  VEFVLCMMPEFYVVLVNFVEAEQDDAT-----VSQLSVILGLANSCANPILYGLFSDNFKR 332
QY      288  FYNKRLKIC 295
Db      333  SFQRT-LC 339

```

RESULT 14

angiotensin I receptor type 1 - bovine
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C:Accession: S15403
 R:Sasaki, K., Yamano, Y., Bardhan, S., Iwai, N., Murray, J.J., Hasegawa, M., Matsuda,
 Nature 351, 220-223, 1991
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angio-
 A:Reference number: S15403; MUID:91251900; PMID:2041569
 A:Accession: S15403
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
 C:Superfamily: vertebrate rhodopsin

Query Match	16.48;	Score 304.5;	DB 2;	Length 359;
-------------	--------	--------------	-------	-------------

Matches 81; Conservative 68; Mismatches 143; Indels 33; Gaps 8;

QY 17 VMPPLIVAFVLGALGNVALGCEFHMKTWKPSVYLENLAVADFLMICLPRTDYLL 76

Db 30 MIP^TLYSIIFVVGIFGNSLVVIVIFYMKLKTVASVFLLNLALADLCFLLTLPWAVYTA 89

77 RRRHWAEGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHPHHA VNTISTRAAGIV 136

Db 90 MEYRWPEGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMS-RLRRTMLVAKVT 148

137 C-TLMALVILGTVLL-ENHLCVQETA VSCSEFIMESANGWHDIMFQLE-----FEMPL 1899

Db 149 CIIMWLAGLASPTIIHRNVEIENTNITVCAFHYESQNSTLPVGLGJTKNIGFLFPF 208

190 GILLECFKI VMSLR RRRQQLARQARMKKATRFIMVAIV--FITCYLP---SVSARLYF 243

DB 209 -LILTSYTLWKTLKKA YEIQKNKPRKDDIFKII LAI V L F F F S W V P H Q I F T E M D V L I Q 267

244 LWTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPSFPEFY-----289

Db 268 LGLIRDKIEDIVDTAMPITICLAYFNCLNPLYGFLGKKFKKYFLQLLKYIPPKAKSH 327

QY 290 ----NKLKICSLKPKQPGHSTQRP 310

D6 328 SNLSTKMSTLSYRPSNGNSSSTKKP 352

RESULT

somatostatin receptor 2 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
 C:Accession: B41795
 R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
 P:Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors
 A:Reference number: A41795; MUID:92108031; PMID:1346068
 A:Accession: B41795
 A:Molecule type: DNA
 A:Residues: 1-369 <YAM>
 A:Cross-references: GB:801830; NID:g307435; PIDN:AAA58248.1; PID:g307436
 A:Note: sequence extracted from NCBI backbone (NCBI:74769, NCBI:74770)
 C:Genetics:
 A:Gene: GDB:SSFR2
 A:Cross-references: GDB:134186; OMIM:182452
 A:Map position: 17q24-17q24

A: Introns: #status absent
 C: Superfamily: Vertebrate rhodopsin
 C: Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pnc
 F: 44-69/Domain: transmembrane #status predicted <TM1>
 F: 80-105/Domain: transmembrane #status predicted <TM2>
 F: 117-138/Domain: transmembrane #status predicted <TM3>
 F: 158-180/Domain: transmembrane #status predicted <TM4>
 F: 205-235/Domain: transmembrane #status predicted <TM5>
 F: 254-281/Domain: transmembrane #status predicted <TM6>
 F: 288-315/Domain: transmembrane #status predicted <TM7>
 F: 9,22,28,32,35/Binding site: carboxylate (Asn) (covalent) #status predicted
 F: 115-193/Disulfide bonds: #status predicted
 F: 250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F: 328/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 16.3%; Score 302.5; DB 2; Length 369;

Best Local Similarity 29.8%; Pred. No. 2.4e-20;
 Matches 90; Conservative 50; Mismatches 135; Indels 27; Gaps 9;

```

QY 13 TRSQVMPPLLIVAFVIGALGNGVALCGFCFHMKTWRKSTVYLLENLAVADFLMIGLCPRT 72
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 41 TSNAYLFTIFYVYVCIIGLCGNLIVYILRYAKMKTTINIIYILNLAIADFLMIGLPLA 100
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 73 DYLRRRHMAEGDIPCRVGLFTLANNRAGSIVFTVAADRYEKVYVHPHNAVNTISTRVA 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 -MQVALVHMPFEGKALCRVVMVDGINQFTSIFCLTVMSIDRYLAVVHPTKSAKMRPRRTA 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 133 AGIVCTIN--LVTLG--TVYLLENHLCVQETAVSCSFIMESANGWHD---IMFQLE 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 160 KNTMAVWGVSILVTLPLTMIYAGLRN--QWGRSSCTINMPGESGAWYTGFIITYTFLIG 216
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

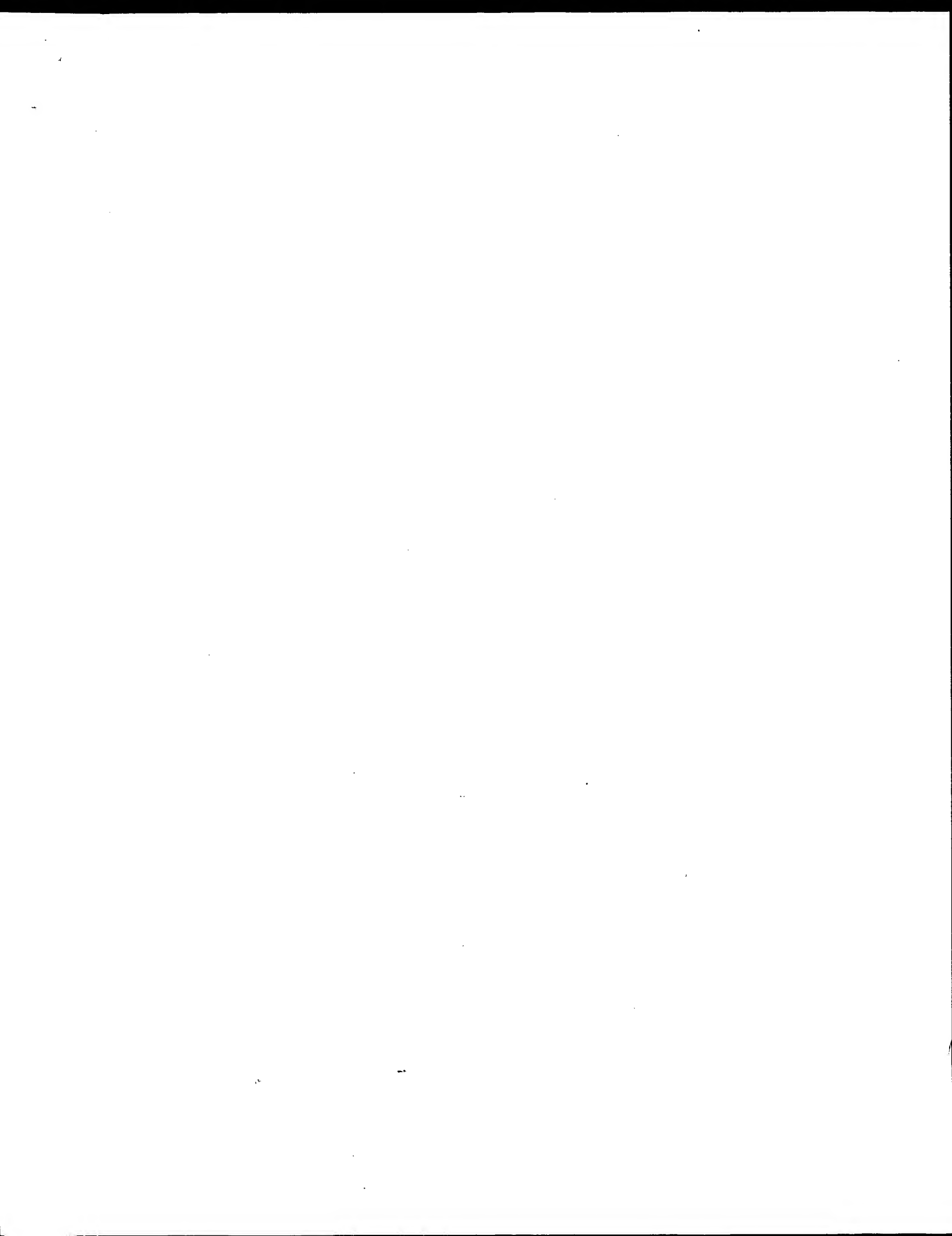
QY 185 FEMPIGITILFCSTIWSLR---RQQLARQARKKATREFIMVVAIVFTCYLPSVSAR 240
   | : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : |
Db 217 FLVPLITICLCFLTIIVKSSGIRVSSKRKSKKATRWASTIVAVFICWLP----- 271
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 241 LYELTWPSASAC---DPSVGHALHTLSFTYMSMDPLVYFSSPSPFKFYNKLIKCS 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 272 -FYIFNVSSVSMASISPTALKGMFDVYVVLTYANSCANPIIYAFSLDNFKKSFQNV-LCL 329
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 297 LK 298
   : |
Db 330 VK 331
   : |

```

Search completed: March 26, 2003, 19:39:12
 Job time : 21 secs



GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:29:48 ; Search time 26 Seconds

(without alignments)
551.954 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853
Sequence: 1 MYNCSGCRTEGDTISQVMP.....ANSFQSQSDGQWDEHIVEMH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	880.5	47.5	387	1	HM74_HUMAN
2	448.5	24.2	319	1	GP31_HUMAN
3	371.5	20.0	309	1	CLT2_MOUSE
4	366.5	19.8	346	1	CLT2_HUMAN
5	364	19.6	362	1	P2YR_CHICK
6	364	19.6	362	1	P2YR_METGA
7	362.5	19.6	373	1	P2YR_BOVIN
8	362	19.5	345	1	CLT2_PIG
9	358.5	19.3	373	1	P2YR_RAT
10	355.5	19.2	309	1	CLT2_RAT
11	354	19.1	373	1	P2YR_HUMAN
12	351.5	19.0	373	1	P2YR_MOUSE
13	346.5	18.7	370	1	P2YR_HUMAN
14	339	18.3	308	1	P2Y5_CHICK
15	336	18.1	367	1	GP17_HUMAN
16	327	17.6	309	1	GP35_HUMAN
17	324	17.5	344	1	P2Y5_HUMAN
18	320	17.3	374	1	P2Y2_MOUSE
19	316.5	17.1	374	1	P2Y2_RAT
20	310.5	16.8	420	1	PAR1_XENLA
21	309.5	16.7	363	1	SSR2_RAT
22	308.5	16.6	307	1	GP35_MOUSE
23	308	16.6	340	1	CLT1_PIG
24	307	16.6	391	1	SSR1_MOUSE
25	305.5	16.5	391	1	SSR1_HUMAN
26	305.5	16.5	391	1	SSR1_MOUSE
27	305	16.5	337	1	CLT1_HUMAN
28	305	16.5	377	1	P2Y2_HUMAN
29	304.5	16.4	359	1	AG2R_BOVIN
30	302.5	16.3	369	1	SSR2_HUMAN
31	302	16.3	391	1	BRB2_HUMAN
32	302	16.3	399	1	PAR2_MOUSE
33	300.5	16.2	369	1	SSR2_MOUSE

34	300.5	16.2	369	1	SSR2_RAT	P30680	rattus norv
35	300	16.2	328	1	P2Y6_RAT	O63371	rattus norv
36	300	16.2	384	1	SSR4_RAT	P30937	rattus norv
37	300	16.2	428	1	SSR3_MOUSE	P34995	mus musculu
38	299.5	16.2	369	1	SSR2_PIG	P34994	sus scrofa
39	299	16.1	388	1	SSR4_HUMAN	P31391	homo sapien
40	299	16.1	397	1	PAR2_RAT	O63645	rattus norv
41	298.5	16.1	418	1	SSR3_HUMAN	P32745	homo sapien
42	298.5	16.1	432	1	PAR1_RAT	P26824	rattus norv
43	298	16.1	375	1	GP34_MOUSE	O9916	mus musculu
44	298	16.1	428	1	SSR3_RAT	P30936	rattus norv
45	297	16.0	397	1	PAR2_HUMAN	P55085	homo sapien

ALIGNMENTS

RESULT 1	HM74_HUMAN	STANDARD:	PRT:	387 AA.
ID	HM74_HUMAN			
AC	P49019:			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Probable G protein-coupled receptor HM74.			
GN	HM74.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RX	MEDLINE=94092629; PubMed=7505609;			
RA	Nomura H., Nielsen B.W., Matsushima K.;			
RT	"Molecular cloning of cDNAs encoding a LD78 receptor and putative			
RT	leukocyte chemotactic peptide receptors.";			
CC	Int. Immunol. 5:1239-1249(1993).			
CC	-1- FUNCTION: ORPHAN RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: D10923; BAF01721.1; -			
DR	HSSP: P34966; 1DDO.			
DR	MIM: 606039;			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	InterPro: IPR001230; Prenyl_site.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PROSITE: PS00237; G-PROTEIN_RECPT_FL1; 1.			
DR	PROSITE: PS00262; G-PROTEIN_RECPT_FL2; 1.			
KW	G-protein coupled receptor; Transmembrane.			
FT	DOMAIN 1			
FT	TRANSMEM 29..58			
FT	DOMAIN 1 (POTENTIAL).			
FT	TRANSMEM 51..63			
FT	DOMAIN 2 (POTENTIAL).			
FT	TRANSMEM 64..85			
FT	DOMAIN 3 (POTENTIAL).			
FT	TRANSMEM 86..102			
FT	DOMAIN 4 (POTENTIAL).			
FT	TRANSMEM 103..123			
FT	DOMAIN 5 (POTENTIAL).			
FT	TRANSMEM 124..143			
FT	DOMAIN 6 (POTENTIAL).			
FT	TRANSMEM 144..163			
FT	DOMAIN 7 (POTENTIAL).			
FT	TRANSMEM 164..194			
FT	DOMAIN 8 (POTENTIAL).			
FT	TRANSMEM 195..209			
FT	DOMAIN 9 (POTENTIAL).			
FT	TRANSMEM 210..236			
FT	DOMAIN 10 (POTENTIAL).			
FT	TRANSMEM 237..256			
FT	DOMAIN 11 (POTENTIAL).			
FT	TRANSMEM 257..273			
FT	DOMAIN 12 (POTENTIAL).			
FT	TRANSMEM 274..298			

[illegible]

GN CYS1LR2 OR CYS1LR2 OR CYS1LR2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteheria; Primates; Catarrhini; Hominiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=placenta;
 RX MEDLINE=20374466; PubMed=10913337;
 RA Takaaski J., Kanohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
 RA Nishikawa T., Kawai Y., Masuno Y., Isogai T., Suzuki Y., Sugano S.,
 RA Furuchi K.;
 RT "The molecular characterization and tissue distribution of the human
 RT cysteinyl leukotriene CysLT2 receptor";
 RL Biochem. Biophys. Res. Commun. 274:316-322(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20459128; PubMed=10851239;
 RA Helise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
 RA Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
 RA Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
 RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
 RA Lynch K.R., Evans J.F.;
 RT "Characterization of the human cysteinyl leukotriene 2 receptor.";
 RL J. Biol. Chem. 275:30531-30536(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20545741; PubMed=11093801;
 RA Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
 RA Civelli O.;
 RT "Molecular cloning and characterization of a second human cysteinyl
 RT leukotriene receptor: discovery of a subtype selective agonist.";
 RL Mol. Pharmacol. 58:1601-1608(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Dunn M.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 17-346 FROM N.A.
 RA Suga H.;
 RL "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system. Stimulation by BAY u9773, a
 CC partial agonist, induces specific contractions of pulmonary veins
 CC and might also have an indirect role in the relaxation of the
 CC pulmonary vascular endothelium. The rank order of affinities for
 CC the leukotrienes is LTC4 > LTD4 > LTE4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 CC heart, placenta, spleen, peripheral blood leukocytes and adrenal
 CC gland. In lung, expressed in the interstitial macrophages, and
 CC slightly in smooth muscle cells.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----
 DR EMBL: AB038269; BAB03601.1; -
 DR EMBL: AF254664; AAG17281.1; -
 DR EMBL: AF279611; AAK69485.1; -
 DR EMBL: AL137118; CAC29102.1; -
 DR EMBL: AB041644; BAB16379.1; -
 DR MIM: 605666; -
 DR InterPro: IPR004071; CysLeuk_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS; PRO1533; CYSLTRECPT.
 DR PROSITE; PS00237; GPCR RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; FALSE NEG.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 42
 FT TRANSMEM 43 63
 FT TRANSMEM 64 72
 FT TRANSMEM 73 93
 FT TRANSMEM 94 123
 FT TRANSMEM 124 144
 FT TRANSMEM 145 153
 FT TRANSMEM 154 174
 FT TRANSMEM 175 204
 FT TRANSMEM 205 225
 FT TRANSMEM 226 245
 FT TRANSMEM 246 266
 FT TRANSMEM 267 286
 FT TRANSMEM 287 307
 FT TRANSMEM 308 346
 FT DISULFID 111 187
 FT CARBOHYD 20 20
 FT CARBOHYD 26 26
 FT CARBOHYD 30 30
 FT CARBOHYD 181 181
 SQ SEQUENCE 346 AA; 39635 MW; EBS4A4A2DCESEEA CRC64;

Query Match 19.8%; Score 366.5; DB 1; Length 346;
 Best Local Similarity 29.9%; Pred. No. 1e-18;
 Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

QY 3 NSGCCAIEDDTISQVMPRLIYAFVYALGNGVALCGCFHMKTKPST--VYLFNLAV 59
 DB 27 NSNRCTIE-NKREFFPIYLLIIFEWGIVGNGISLIVF---LQPKKSTSVNVMNLAI 82
 QY 60 ADELIMICPFRTDYLRBRHNAFGDIPCRVGFETLAMRAGSIVFLTVADRFKVVH 119
 DB 83 SLLFLSTLPFRADYLRKSNMIFGDLACRISYSLVYMNSSITFLVLSVFRFLAVH 142
 QY 120 PHHAVNTISTRAAGIVCTMALVLTIGTYLLLENHLCVOETAVSC--ESFIMESANGW 176
 DB 143 PERLLHVTISR-SAMILCGIIMLIMWASSIMLLDSENGSVTSCLELTKIAKLTQM 201
 QY 177 HDIMPLEFFMPLGIIIFCSFKIWSLRKQ--QLARQARKAKATRFIMVAIVITCYL 234
 DB 202 NITALVVGCLLPFTLSTICYLLIIRVLKVEVESEGLRVSHRKALTTIITLILFELCP 261
 QY 235 PVSARLVEFLMTVPSSACDPVSHGALHILTSFYMNMSMDPIVYFESSPSPKFKYKIKI 294
 DB 262 PHTLTFTVHLTTWKVGLCKDRHLKALVITLALANACNPPLTYFAGENK--DRUK- 317
 QY 295 CSLKPKOPGHSKTQ 308
 DB 318 SALRKGHPOKAKTK 331
 RESULT 5
 P2YR_CHICK STANDARD: PRT: 362 AA.
 AC P3496;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinoergic receptor).
 GN P2RY1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE=93285340; PubMed=8508924;
 RA Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
 RA King B.F., Burnstock G., Barnard E.A.;
 RT "Cloning and functional expression of a brain G-protein-coupled ATP
 RT receptor.";
 RL FEBS Lett. 324:219-225(1993).
 RP [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=97026278; PubMed=8872457;
 RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
 RT "Modelling the P2Y purinoceptor using rhodopsin as template.";
 RL Drug Des. Discov. 13:133-140(1995).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
 CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERUSSIS TOXIN
 CC INSENSITIVE G-PROTEIN. PROBABLY BELONGING TO THE GQ FAMILY THAT
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT,
 CC STOMACH, LUNG AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@ebi.ac.uk).

CC EMBL: X73268; CAAS1716.1; -
 DR PIR: S33733; S33733.
 DR PDB: IDDD: 1J-JUL-96.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCR RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
 FT DOMAIN 1 41
 FT TRANSMEM 42 63
 FT TRANSMEM 64 76
 FT TRANSMEM 77 98
 FT TRANSMEM 99 115
 FT TRANSMEM 116 136
 FT TRANSMEM 137 155
 FT TRANSMEM 156 177
 FT TRANSMEM 178 207
 FT TRANSMEM 208 227
 FT TRANSMEM 228 254
 FT TRANSMEM 255 274
 FT TRANSMEM 275 292
 FT TRANSMEM 293 317
 FT TRANSMEM 318 362
 FT TRANSMEM 362 391
 FT DISULFID 111 191
 FT CARBOHYD 11 11
 FT CARBOHYD 26 26
 FT CARBOHYD 102 102
 FT CARBOHYD 186 186
 SQ SEQUENCE 362 AA; 41194 MW; A80C88FB9514761 CRC64;

Query Match 19.6%; Score 364; DB 1; Length 362;
 Best Local Similarity 29.1%; Pred. No. 1.5e-18;
 Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

QY 18 MPRLIYAFVYALGNGVALCGCFHMKTKPSTVYLFNLAVADFLIMCLPRTDYLR 77
 DB 43 LPTVYLVFTIGLGNVAIWMFVFMHWPWSGISYVMFNALADFLYVLTLPFIYFN 102
 QY 78 RHHAFSGDIPCRVGFETLAMRAGSIVFLTVADRFKVVHHAHVNITSTRVAAGIYC 137
 DB 103 KTDWIFGDMCKLQRFLEHVNLYGSLIFLTGISVHRYGVVHPLKSLGRKKNNAVYSS 162

Query Match	Best Local Similarity	Score 364;	DB 1;	Length 362;
Matches 95;	Conservative 58;	Mismatches 130;	Indels 44;	Gaps
FT TRANSMEM	42	63	1 (POTENTIAL).	
FT DOMAIN	64	76	CYTOPLASMIC (POTENTIAL).	
FT TRANSMEM	77	98	2 (POTENTIAL).	
FT DOMAIN	99	115	EXTRACELLULAR (POTENTIAL).	
FT TRANSMEM	116	136	3 (POTENTIAL).	
FT DOMAIN	137	155	CYTOPLASMIC (POTENTIAL).	
FT TRANSMEM	156	177	4 (POTENTIAL).	
FT DOMAIN	178	207	EXTRACELLULAR (POTENTIAL).	
FT TRANSMEM	208	227	5 (POTENTIAL).	
FT DOMAIN	228	254	CYTOPLASMIC (POTENTIAL).	
FT TRANSMEM	255	274	6 (POTENTIAL).	
FT DOMAIN	275	292	EXTRACELLULAR (POTENTIAL).	
FT TRANSMEM	293	317	7 (POTENTIAL).	
FT DOMAIN	318	362	CYTOPLASMIC (POTENTIAL).	
FT DISULFID	113	191	BY SIMILARITY.	
FT CARBOHYD	11	26	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	26	26	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	102	102	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ SEQUENCE	362 AA;	41180 MW;	3EL28AB9EB64349C CRC64;	
Query Match	19.6%;	Score 364;	DB 1;	Length 362;
Best Local Similarity	29.1%;	Pred. No. 1.5e-18;		
Matches 95;	Conservative 58;	Mismatches 130;	Indels 44;	Gaps
DB 18	MPPLILVAVFVIGALNGVALGCFCHMKRWKSTYYLFLNLANADFLMLCLFFRDYYLR	77		
DB 43	LETFVILVFITFLNLSVAIMFVHMRWGSISVYMFLADFLVYTLTFLALFYFFN	102		
QY 78	RRHMAFGDIPICVGLFTTAMNAGSIVFLTVAADRFVFNPHAAVNTISRVAAGIYC	137		
DB 103	KIDWJEGDWCKLQRFIFVHNLVGSILFELTCSVHRITGVVHPLKSLGKRRKNVYSS	162		
QY 138	TLMALVIL-----GTVYLLFNHLUCVETA-----VSCSEFIMESANGWHD	178		
DB 163	IWMALVAVAVIADILFYSGGVGRNMTITCYDTPADEYLRKYVYSMCTVFM-----	214		
QY 179	IMEOLFEPMLDILIFCSFKIWSRRROQLARQAMKATRFINWVAIVFTCYLP---	235		
DB 215	-----FCFPEFVILGCGGLVAKILYK-DLDNSPLRKSILYLVITLVFAVSTILPFHV	267		
QY 236	-----SVSARLYFLMTVPSSACDPVSHALHTLTSFTYNNMSMDPLVYVFSSESPFKFYK	291		
DB 268	MKTLMRLARLDF-QRPOMCAFMNDKYYATVQYTRGLASINSCVDPLVFLAGDTFFRRLSR	326		
QY 292	IKICSLKPKOPSHKTOPREKPIISL 318			
DB 327	ATRKSRKSRSE--NWQSKSEKTLNILL 351			
RESULT 7				
P2YR_BOVIN	STANDARD;	PRT;	373 AA.	
ID P2YR_BOVIN	P48042;			
DT 01-FEB-1996	(Rel. 33, Created)			
DT 01-FEB-1996	(Rel. 33, Last sequence update)			
DT 15-JUN-2002	(Rel. 41, Last annotation update)			
DE P2Y purinoceptor 1	(ATP receptor) (P2Y1) (Purinergic receptor).			
GN P2RY1.				
OS Bos taurus (Bovine).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC Bovidae; Bovinae; Bos.				
OX NCBI_TaxID=9913;				
RN [1]				
RN SEQUENCE FROM N.A.				
RC TISSUE=Arctic endothelium;				
RX MEDLINE=95352058; PubMed=7626079;				
RA Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;				
RL "Cloning and Characterisation of a bovine P2Y receptor.";				
RT Biochem. Biophys. Res. Commun. 212:448-656(1995).				
RN [2]				
RN SEQUENCE FROM N.A.				

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RC TISSUE=Corpus callosum;
RA MEDLINE=99064562; PubMed=9848096;
RA Deng G., Maute C., Kumar C., Fogarty D.J., Miledi R.;
RT "Cloning and expression of a P2y purinoceptor from the adult bovine
RL corpus callosum."
CC Neurobiol. Dis. 5:259-270(1998).
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X87628; CAA60958.1; -.
DR EMBL: U34041; AAC78275.1; -.
DR HSSP: P34996; IDDD.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42287 MW; 9270A7175C0BD476 CRC64;

Query Match 19.6%; Score 362.5; DB 1; Length 373;
Best Local Similarity 27.5%; Pred. No. 2e-18;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

QY 18 MPPLIAVAVLQALNGVALCGFCFHKMTKPRSTYVLPRLAVADLMLICLPRFDYLR 77
DB 54 LPAVYLVVIFLIGLSVAIMFVPHMKPWSGISVYMFLADLVLVLPALFYFN 113
QY 78 RRMHAGDIPRCVGLPTLMMNRAGSIVFLTVAAADRYEVPHHAIVTISTRVAGIVC 137
DB 114 KIDMIFGDMACKLQRFIFVHNLXGSLFLPTCSAHRKSSVYVPLSLGRLKKNVYISV 173
QY 138 TMAVYVLTGYVLLLENHLCVQET-AVSC-----ESPTMESANGMDIMFQLEFEM 187
DB 174 LVMLIVVAGISPLIFYSGIGIRKRNKTYTDTSDSEYLSEYFIYSM-----CTVAMFCV 228
QY 188 PLGIIIFGCFKIVMSLRKQQLARQARKKATRFIMVVAIVITCYLP-----SVAR 240
DB 229 PLVLIGCGGLVRLALIV-DLDNSPLRKRSIYLVILVTVAVSYIPFHVAKTNLRLAR 287
QY 241 LVFLMTVPSSACDPVHAGLHLITLSPFYNSMLDPLVYVFFSSPPKFKYKLIKLSLKP 300
DB 288 LDF-OTPEKAFNDKRYATYQVTRGLASLNSCVDPLIVFLAGDTTRRLSR----- 337

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QY 301 QPGHKTQREMPISNLGRSCISVANSFQSGSD 335
DB 338 -ATKRRSRSEANLQSKSEMDTLITSEPKONGD 370

RESULT 8
CLUT2_PIG STANDARD; PRT; 345 AA.
AC 095N03;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Cysteinyl leukotriene receptor 2 (CysLTR2).
GN CysLTR2 OR CysLTR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_Taxid=9823;

RP SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushima H., Furuchi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
RL receptors."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB052662; BAB60817.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; FALSE_NEG.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 1 (POTENTIAL).
FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 94 2 (POTENTIAL).
FT DOMAIN 95 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 145 3 (POTENTIAL).
FT DOMAIN 146 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 246 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 247 267 6 (POTENTIAL).
FT DOMAIN 268 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 345 CYTOPLASMIC (POTENTIAL).
FT DISULFID 112 188 BY SIMILARITY.
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 345 AA; 39410 MW; 5D1B1FB89B95905 CRC64;

Query Match 19.5%; Score 362; DB 1; Length 345;
Best Local Similarity 31.3%; Pred. No. 2e-18;
Matches 86; Conservative 59; Mismatches 118; Indels 12; Gaps 5;

QY 19 MPPLIAVAVLQALNGVALCGFCFHKMTKPRST---VYLFNLAVADLMLICLPRFDY 75

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Db 43 PIVLVLEIFMGALNGSFIVF---LKPYSKSTSVNFMNLAIISDLFTLITLPERDYD 99
QY 76 LRRHNAFGDIPCRVGLFTLAMNAGSIVLTVAADRYKVVHPHNAVNTSTRVAGI 135
Db 100 LRGSNXLFGDPCPKIMSYVMVNMYSISVLTVAADRYKVVHPHNAVNTSTRVAGI 158
QY 136 VCTMALVILGTVYLLLENHLCVOETAVSC---ESFIMESANGHMDIMFQLEPFMGI 192
Db 159 LCGVWIFIMASSVTLKNGSEKDNVTLCLLELNSKNTKTKMNYVALYVGVLPGL 218
QY 193 LFGSKVWISRRROQLARQARM--KKAATRFVVAIVFTCYLPSVASRLYFLWVPS 250
Db 219 SICVLLIRALLKVEVPESGRLSHRRKALLTVIILITFLICLPYHVLRTLHLEKAD 278
QY 251 ACDPSVGHALHTLSTFYNMNMDPLVYFSSPSF 285
Db 279 KCKDRLHKAVALTLAANAANSCFNPFLYFAGENE 313

RESULT 9
P2YR_RAT STANDARD; PRT; 373 AA.
ID P2YR_RAT
AC P49651;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE P2Y purinoreceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=95298025; PubMed=7779087;
RA Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT Cloning of rat and mouse P2Y purinoreceptors.
RL Biochem. Biophys. Res. Commun. 211:211-218(1995).
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS
CC OF EXTRACELLULAR ATP ON INSULIN SECRETION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,
CC LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U22830; AAA91303.1; -
DR HSSP: P34996; 1DDP.
DR Interpro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPT_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52
FT TRANSMEM 53 74
FT DOMAIN 75 87
FT TRANSMEM 88 109
FT DOMAIN 110 126
FT TRANSMEM 127 147
FT DOMAIN 148 166
FT TRANSMEM 167 188
FT DOMAIN 189 218
EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 219 238
FT DOMAIN 239 265
FT TRANSMEM 266 285
FT DOMAIN 286 303
FT TRANSMEM 304 328
FT DOMAIN 329 373
FT DISULFID 124 202
FT CARBOHYD 11 11
FT CARBOHYD 27 27
FT CARBOHYD 113 113
FT CARBOHYD 197 197
SQ SEQUENCE 373 AA; 42321 MW; 6DDF676287B5648 CRC64;

Query Match
Best Local Similarity 27.0%; Score 358.5; DB 1; Length 373;
Matches 91; Conservative 68; Mismatches 139; Indels 39; Gaps 8;

QY 18 MPVLIVAVLALNGVLCGCEFHMKTKSTVYLFENLAVADFLMIGLPFRDYLR 77
Db 54 LPVAVLVLEIFLGISVSAIWMFVFMKPKWSGISVYMFNLADLVYITLIPALFYFN 113
QY 78 RRRHNAFGDIPCRVGLFTLAMNAGSIVLTVAADRYKVVHPHNAVNTSTRVAGI 137
Db 114 KTDWIFGDVWCKIORFIFVNLGSLIFLCISARHYSGVVPLKSLGKKKNAIYVS 173
QY 138 TLMALVILGTVYLLLENHLCVOET-AVSC-----ESFIMESANGHMDIMFQLEPFM 187
Db 174 LWMILVAVLISPLFYSGTGIRKNTVCTDSTDSBYLRSTYISM-----CTVAMFCI 228
QY 188 PLGILFSEFKIVWSLRRROQLARQARMKKAATRFVVAIVFTCYLP-----SVSAR 240
Db 229 PVLVLICGGLVRLVLYR-DLNSPLRKSLYIVLVTVAVSYIFPHWKTNNLAKR 287
QY 241 LPLVLTWPSSACD--PSVGHALHTLSTFYNMNMDPLVYFSSPSFPEYKLGICSLK 298
Db 288 LDF---QTPEMCDPNDRYATYQVTRGLASLNSCDPLIYFAGDTFRRLSR----- 337
QY 299 PKOPGSKTQREEMPISNLGRSCISVANSROSQSD 335
Db 338 -----ATRKASRSEANLQSKSEMTLNLISERKQND 370

RESULT 10
CLT2_RAT STANDARD; PRT; 309 AA.
ID CLT2_RAT
AC Q924T9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Cysteinyln leukotriene receptor 2 (CysLTR2) (RSBP132).
GN CysLTR2 OR CysLTR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushime H., Furutachi K.;
RT Characterization of the cloned rat and porcine cysteinyl leukotriene
RT receptors.
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC EMBL: AB052661; BAB60816.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; FALSE_NEG.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT TRANSMEM 48 56
 FT TRANSMEM 57 77
 FT TRANSMEM 78 98
 FT TRANSMEM 99 119
 FT TRANSMEM 120 137
 FT TRANSMEM 138 158
 FT TRANSMEM 159 187
 FT TRANSMEM 188 208
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 FT TRANSMEM 230 250
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 FT TRANSMEM 564 580
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 FT TRANSMEM 632 648
 FT TRANSMEM 649 665
 FT TRANSMEM 666 682
 FT TRANSMEM 683 699
 FT TRANSMEM 700 716
 FT TRANSMEM 717 733
 FT TRANSMEM 734 750
 FT TRANSMEM 751 767
 FT TRANSMEM 768 784
 FT TRANSMEM 785 801
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 FT TRANSMEM 1703 1719
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 FT TRANSMEM 1737 1753
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Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
18 MBELLIVAFVGLANGVALGCGCFCHMKTKWKSSTVLENLVAADPLMLCIPFRIDYLR	19.0%; Score 351.5; DB 1; Length 373;	91;	66;	143;	35;	8;
54 LPAVYLIVLEIFIGLGSVAIMFVFMHMKWGISIVYEMFLADPLVLTPLLIFYTN	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
78 RHHMAFGDIPCCVNGLETTLMAINRAGSIVLETTVAADRYEFVVRPHNAVNTISTRVAAGIYC	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
114 KIDWIFGDMCKLQRFIFVNLXGSLFELTICSAHNSGVVPRDKSLGGLKKNALIVSV	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
138 TLMALVIGTVLLLENHLVQGET-AVSCSEFTMESANGMHDIMFOLE-----FMPL	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
174 LVMLIVVAVISPILFEYSGETGRKNKTVTCYD--TTSNDYLSRYFIYSMCTVAMCIP	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
190 GIIFCFSFITYWSLRRODLARQARKKATRTLMVAIVIFITCYP-----SVSARLY	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
231 VLLICGGLIVKAL-IYNLDNPSPLRKRSIYLVIIIVTFEAVSYIPFHMKTMMNLEARD	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
243 FLMTVPSSACD--PSVHGALHTLTSFTYNSMLDPLVYFSSPFPKFNKLKICSLKPK	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
290 F---OTPEKCDNDKRYATIVYTRGIASLNSCYVDPLVIFLAGDTRRLRSR-----	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
301 OPHGSKTORPEEMPISNLGRCSICVANSFOSQSD	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;
338 --ATRKASRSEANLQSKSEMTLNLISLFEKNGD	27.2%; Pred. No. 1.2e-17;	91;	66;	143;	35;	8;

FT	DISUPEFD	111	188	BY SIMILARITY.
FT	CARBOHYD	15	15	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	24	24	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	28	28	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	192	192	F -> L (IN REF. 3).
SO	SEQUENCE	370 AA;	41895 MW;	20857552A3929E48 CRC64;
Query Match				
Best Local Similarity 31.2%; Score 346.5; DB 1; Length 370;				
Matches 95; Conservative 52; Mismatches 128; Indels 29; Gaps 11				
QY	24	VAEVLGALNGVLAJCECFEHMKTWKPSYVLEFNLAADFLMIGLCPEDPTDYLRRHMR	83	
Db	48	VVEILGILTNSSVLSPEFCFRMKMBETALFTINLAASDLLEVCCLLPKRT-FYENRRHMP	106	
QY	84	GDIPCRVGLFTLAMNAGSIVEFLVVAADRYEKVYVPHHNAVNTSTFVAGIYCT-LMAL	142	
Db	107	GDPLKICISGTAFLTNIGSGMLFTICISVDRELAIFYPPRS-RTIRTRNSAIVCAGWML	165	
QY	143	VILGTVLLLEHNLICQVETAVSC-PSFLMESANGHDMFPLE-----FNPDLGILF	194	
Db	166	VISGGISASLFTSTNNNAATTCEGCF--SKRWKITYLSKITTFIEVVGITPLILNVS	222	
QY	195	CSEKIVWSLRRQQLAR-QARRKATREIMVAIVFITCYLPSVSARLPLMTVPSSAC-	252	
Db	223	CSSVLTRELKRPATLSQIGTNKKKVLKMLTGMVAEYVCEPYNVS-VLEFLALVNSQAI	280	
QY	253	-----PPSVHGAHLITLSTFYWNMSLDPLVYFVSSPSPK-FYKKALICSLKROGHSK	306	
Db	281	TNCFLEKPAKIMPTILCLATLNCCEDFPIFYFLESPKSEFYINAH-----RMESLKP	335	
QY	307	TQRP	310	
Db	336	TEMP	339	
RESULT 14				
P2Y5_CHICK	ID	P2Y5_CHICK	STANDARD:	PRT; 308 AA.
AC	P32250;			
DT	01-OCT-1993 (rel. 27, Last sequence update)			
DT	01-OCT-1993 (rel. 27, Last sequence update)			
DT	15-JUL-1998 (rel. 36, Last annotation update)			
DE	P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).			
GN	P2RY5.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=T-cell;			
RC	MEDLINE=93329058; PubMed=8393036;			
RX	Kaplan M.H., Smith D.I., Sundick R.S.;			
RT	Identification of a G protein coupled receptor induced in activated			
RT	T cells.";			
RL	J. Immunol. 151:628-636(1993).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	or send an email to license@isb-sib.ch).			
CC	EMBL; L06109; AAB06587.1; -.			
CC	HSSP; P34996; 1DD.			

QY 184 EFMPLGIIIECSFKIWSLRROOLARQRMK-KATRFIMVVAIVFTCYLP-SVSARL 241
 Db 228 AFTFPFITVTCYLLIIRSL-RQGLRVERRLTKAVRMIAIVLAFIVCFVPIHNRSV 285
 QY 242 YFL-WVPPSACDPSYHGAL-HITLSFTYMNMDPLVIYFSSPSFPKFYNKIKICSLK 298
 Db 286 YVLHYNHSHGASCATORILALANRITSLTSLNGALDPIWFFVAEKFRHALCNL-LGGR 344
 QY 299 PKOGHSHKTORPEEMPIS 316
 Db 345 LKGPPSPFEGKTNSSLS 362

Search completed: March 26, 2003, 19:38:05
 Job time : 27 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:35:13 ; Search time 34 Seconds
(without alignments)
2096.832 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853
Sequence: 1 MYN5CRIEGDTISQVMP.....ANSFOSQSDGOWPHIVEMH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	4 Q9BXC0	Q9BXC0 homo sapien
2	883.5	47.7	363	4 Q8TDS4	Q8TDS4 homo sapien
3	868.5	46.9	360	11 Q9EP66	Q9EP66 mus musculu
4	529	28.5	423	4 Q8TDS5	Q8TDS5 homo sapien
5	450.5	24.3	319	4 Q9NQ20	Q9NQ20 homo sapien
6	446.5	24.1	319	11 Q9JLS1	Q9JLS1 mus musculu
7	375.5	20.3	309	11 Q8R528	Q8R528 mus musculu
8	351.5	19.0	390	13 Q8Q604	Q8Q604 carassius a
9	342.5	18.5	357	13 Q9DE05	Q9DE05 raja erinac
10	341	18.4	361	13 Q9QX57	Q9QX57 xenopus lae
11	329.5	17.8	380	13 Q9QD06	Q9QD06 carassius a
12	305	16.5	372	4 Q9H1C0	Q9H1C0 homo sapien
13	303.5	16.4	359	6 Q9N0U1	Q9N0U1 ovis aries
14	302.5	16.3	346	4 Q9G6E0	Q9G6E0 homo sapien
15	302.5	16.3	356	4 Q9GTF2	Q9GTF2 homo sapien
16	300.5	16.2	346	6 Q95KS6	Q95KS6 ovis aries

17	299.5	16.2	346	11 Q91Y73	Q91Y73 mus musculu
18	297	16.0	370	13 Q8UWL5	Q8UWL5 fuqu rubrip
19	297	16.0	399	11 Q8R311	Q8R311 mus musculu
20	293	15.8	315	6 Q9GKP7	Q9GKP7 sus scrofa
21	293	15.8	374	13 Q57466	Q57466 meleagris g
22	293	15.8	385	11 Q9JK40	Q9JK40 mus musculu
23	292.5	15.8	361	6 Q46685	Q46685 bos taurus
24	292	15.8	317	11 Q99MT6	Q99MT6 mus musculu
25	292	15.8	359	6 Q9GLN9	Q9GLN9 pan troglod
26	291.5	15.7	358	4 Q96J28	Q96J28 homo sapien
27	291	15.7	359	11 Q9EP63	Q9EP63 cavia porce
28	290.5	15.7	337	4 Q96P68	Q96P68 homo sapien
29	290.5	15.7	359	11 Q99MT7	Q99MT7 mus musculu
30	289	15.6	343	11 Q9QW32	Q9QW32 ratu sp.
31	288.5	15.6	359	11 Q9E0R9	Q9E0R9 meriones un
32	288	15.5	355	11 Q9JUX8	Q9JUX8 ratu nov
33	287.5	15.5	298	11 Q8VE54	Q8VE54 mus musculu
34	287.5	15.5	358	4 Q9BY21	Q9BY21 homo sapien
35	286.5	15.5	355	4 Q9BYX5	Q9BYX5 homo sapien
36	286.5	15.5	423	5 Q964D4	Q964D4 periplaneta
37	286	15.4	359	4 Q8TRK4	Q8TRK4 homo sapien
38	283	15.3	328	11 Q9ERK9	Q9ERK9 mus musculu
39	282.5	15.2	330	4 Q9BXA5	Q9BXA5 homo sapien
40	282.5	15.2	334	4 Q8TDQ8	Q8TDQ8 homo sapien
41	282	15.2	351	6 Q9MYJ9	Q9MYJ9 oryctolagus
42	279	15.1	392	6 Q9BDQ4	Q9BDQ4 canis famill
43	278.5	15.0	355	11 Q91VP9	Q91VP9 mus musculu
44	278.5	15.0	383	13 Q42324	Q42324 calostomus
45	275	14.8	377	13 Q98U14	Q98U14 brachydanio

ALIGNMENTS

RESULT 1
Q9BXC0 PRELIMINARY; PRT; 346 AA.

AC Q9BXC0: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative chemokine receptor (G protein-coupled receptor) (Putative
DE G-protein coupled receptor)
GN FKS680 OR GPR81 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Y.-g, Gong L.;
RT "Molecular cloning of FKS680, a novel gene encoding a putative
RT chemokine receptor.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Yanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF345568; AAK29071.1; -
DR EMBL: AF411110; AAL26481.1; -
DR EMBL: AB083631; BAB9344.1; -
DR HSSP: P34996; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SO SEQUENCE 346 AA; 39295 MW; E0DB114EEB3A47A5 CRC64;

Query Match 100.0%; Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1,1e-174;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGSCCRLEGDTISQVMPPLIVAFVIALGNGVALCGCFCHMKTKWKPSTVYLNLAV 60
 DB 1 MNGSCCRLEGDTISQVMPPLIVAFVIALGNGVALCGCFCHMKTKWKPSTVYLNLAV 60
 QY 61 DFLMCLCPFRDYLYRRRMAFGDIPCRVGLFTLAMNAGSIIVFTLVAAADRYKVHP 120
 DB 61 DFLMCLCPFRDYLYRRRMAFGDIPCRVGLFTLAMNAGSIIVFTLVAAADRYKVHP 120
 QY 121 HNAVNTSTRVAGIVCTMALVILGTVYLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 DB 121 HNAVNTSTRVAGIVCTMALVILGTVYLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFMPGLILFCSEFKIWSLRROQLARQARKKATRTIMVAIVFTICLPSVSAR 240
 DB 181 FOLEFMPGLILFCSEFKIWSLRROQLARQARKKATRTIMVAIVFTICLPSVSAR 240
 QY 241 LYELMTVPSSACDPVHGALHTLSTFTYNSMLDPLVYFSSPFPKFNKLKICSLRK 300
 DB 241 LYELMTVPSSACDPVHGALHTLSTFTYNSMLDPLVYFSSPFPKFNKLKICSLRK 300
 QY 301 QPCHSKTORPEEMPISNLGRSCISVANSFOSQSDGQMPHIVEMH 346
 DB 301 QPCHSKTORPEEMPISNLGRSCISVANSFOSQSDGQMPHIVEMH 346

RESULT 2

Q8TDS4 PRELIMINARY; PRT; 363 AA.
 AC Q8TDS4;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Putative G-protein coupled receptor.
 GN GPCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT Identification of G protein-coupled receptor genes from the human
 RT genome sequence.";
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB083632; BAB89345.1; -;
 KW Receptor.
 SO SEQUENCE 363 AA; 41849 MW; CAB0EBC9CCB81D56 CRC64;

Query Match 47.7%; Score 883.5; DB 4; Length 363;
 Best Local Similarity 52.8%; Pred. No. 6e-79;
 Matches 180; Conservative 47; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCCRIGDTISQVMPPLIVAFVIALGNGVALCGCFCHMKTKWKPSTVYLNLAVADFL 64
 DB 17 NCCVDFDIIVKLPVYLLEFLIGLNGALMIFCFHLKSKMSRIFLFNLAADELL 76
 QY 65 MCLPRTDYLYRRRMAFGDIPCRVGLFTLAMNAGSIIVFTLVAAADRYKVHPHNAV 124
 DB 77 ICLPFLMNVYVRMDKMGDIPCRVGLFTLAMNAGSIIVFTLVAAADRYKVHPHNAV 136
 QY 125 NTSTRVAGIVCTMALVILGTVYLLENHLCVOETAVSCSEFIMESANGWHDIMFOLE 184

DB 137 NKISNRATAISCLLWITTLGIVHLILKKMPIONGANGNLCSFSICHTQEWHEAMEFILE 196
 QY 185 FEMPLIGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICLPSVSARLYFL 244
 DB 197 FFLPGLILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICLPSVSARLYFL 255
 QY 245 WTVPSA---CD--PSYHGALHTLSTFTYNSMLDPLVYFSSPFPKFNKLKICSLRK 299
 DB 256 WLHTSGTQNCVEYRVSLAFITLSTFTYNSMLDPLVYFSSPFPKFNKLKICSLRK 315
 QY 300 KQPHSKTORPEEMPISNLGRSCISVANSFOSQSDGQMP 340
 DB 316 KMGEPDNNRSTSVELTGDPNKT-RGAPDALMANSGEWSP 355

RESULT 3

Q9EP66 PRELIMINARY; PRT; 360 AA.
 AC Q9EP66;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Putative seven transmembrane spanning receptor.
 GN PUMA-G.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ, AND C57BL/6;
 RA Schaub A., Fletterer A., Pfeiffer K.;
 RT "PUMA-G, an interferon-gamma inducible gene in macrophages is a novel
 RT member of the seven transmembrane spanning superfamily.";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ300199; CAC17791.1; -;
 DR EMBL; AJ300198; CAC17790.1; -;
 DR HSSP; P34996; 1DDJ.
 DR MGD; MGI:193383; Puma-g.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SO SEQUENCE 360 AA; 41400 MW; CCCES2A2475777FC CRC64;

Query Match 46.9%; Score 868.5; DB 11; Length 360;
 Best Local Similarity 55.6%; Pred. No. 1.8e-77;
 Matches 178; Conservative 39; Mismatches 96; Indels 7; Gaps 4;

QY 3 NG-SCCRIGDTISQVMPPLIVAFVIALGNGVALCGCFCHMKTKWKPSTVYLNLAVAD 61
 DB 11 NGKNCVFRDENIAKVPVYLLEFLIGLNGALMIFCFHLKSKMSRIFLFNLAAVAD 70
 QY 62 FLMCLCPFRDYLYRRRMAFGDIPCRVGLFTLAMNAGSIIVFTLVAAADRYKVHPH 121
 DB 71 FLITICLPFLTDNVVHNMKDRFGICPCRVMLFLAMNAGSIIVFTLVAAADRYKVHPH 130
 QY 122 HNAVNTSTRVAGIVCTMALVILGTVYLLENHLCVOETAVSCSEFIMESANGWHDIM 181
 DB 131 HFLKISNRATAISCLLWITTLGIVHLILKKMPIONGANGNLCSFSICHTQEWHEAMEFILE 190
 QY 182 QLEFMPGLILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICLPSVSARL 241
 DB 191 LLEFPLALILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICLPSVSARL 249
 QY 242 YFLMTVPS---SACD--PSYHGALHTLSTFTYNSMLDPLVYFSSPFPKFNKLKICSLRK 296
 DB 250 RIFMLIKYVNRCDIYSSVDLAFTLSTFTYNSMLDPLVYFSSPFPKFNKLKICSLRK 309

1000

DT 01-MAR-2001 (Tremblrel, 16, Created)
 DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
 DE Putative G protein-coupled receptor 92 (Putative G-protein coupled receptor)
 GN GPR92 OR GPR93 OR GPCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20517346; PubMed=11062477;
 RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-Depierreux B., Grabowski M., Meilinger T., Strom T.M., "Autosomal dominant hypophosphataemic rickets is associated with mutations in FGFR3." Nat. Genet. 26:345-348(2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21458557; PubMed=11574155;
 RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Atkilitko O., Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
 RT "Discovery and mapping of ten novel G protein-coupled receptor genes." Gene 275:83-91(2001).
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Takada S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human genome sequence." Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AL272207; CAC03725.1;
 DR EMBL: AF411112; AAL26483.1;
 DR EMBL: AB083600; BAB9313.1;
 DR HSSP: P34996; 1DDP.
 DR Interpro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 372 AA; 41346 MW; BA35709084BB6D84 CRC64;

Query Match 16.5%; Score 305; DB 4; Length 372;
 Best Local Similarity 29.4%; Pred. No. 7.8e-22;

Matches 91; Conservative 44; Mismatches 125; Indels 50; Caps 10;

QY 13 TISQVMP-----DLIVAFVGLGALG--NGVALGCFCHMKTKPSTVYLFINAV 59
 DB 8 TNSVLPDPRDYRPTNRHLVLYSIVLA--GLPLNALMLVLRALRVHSAVSVMCNLAA 66
 QY 60 ADELMLTCLPRTDYLLRRHMAFGDIPCRVGLFTLANNRAGSIVFLVVAADRYFVHV 119
 DB 67 SDLFTLSLPLVRLSY-ALHHMPDPLLCQTGAIFQNMVSGSCIFMLINVDRYAIVH 125
 QY 120 PHNAVNTSTVRAAGIVCTMAVITGV-----YLLLENHLCVQETAVSCS 167
 DB 126 PLRLRLRRPRVARILCGVALLIVAVPARAVHRSRCRYRDLERVLGF-----ES 178
 QY 168 FIMESANGMHDIMF-----QLEFFMPLGILFCSPKIYVSLRRQOLARQARKKATR 220
 DB 179 F---SDELMKGRLLPLVLLALGFLPLPLAAVYSSGRVFETLARPRATQSQ--RRKTVR 234
 QY 221 FIMVAIVFICYP-----SVSARLYFLMTVPSSACDPVHGALHTLSTFTYNSMLDP 275
 DB 235 LLNLNLVFLLCFVYNTSLAVYGLRSKIVAAVSPARDRVGLVAVMLAGANCVLDP 294
 QY 276 LVYFSSPSF 285
 DB 295 LVYFSAAGF 304

RESULT 13
 ID 09N001 PRELIMINARY; PRT; 359 AA.
 AC 09N001;
 DT 01-OCT-2000 (Tremblrel, 15, Created)
 DT 01-OCT-2000 (Tremblrel, 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel, 20, Last annotation update)
 DE Angiotensin II type 1 receptor.
 OS Ovis aries (sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
 NCBI_Taxid=9940;
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADRENAL CORTEX;
 RA Bird I.M., Milligan D.S.;
 RT "Isolation of a full length ovine Angiotensin II Type-1 Receptor (AT1-R) cDNA." Endocr. Res. 0:0-0(2000).
 RL [1]
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF254119; AAF6063.1;
 DR HSSP: P34996; 1DDP.
 DR Interpro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 359 AA; 41062 MW; C07010EDB8110EB CRC64;

Query Match 16.4%; Score 303.5; DB 6; Length 359;
 Best Local Similarity 24.9%; Pred. No. 1.1e-21;

Matches 81; Conservative 68; Mismatches 143; Indels 33; Gaps 8;

QY 17 VMPDLIVAFVGLGALGNGVALGCFCHMKTKPSTVYLFINAVADFLMICLPFTDYLL 76
 DB 30 MIPLYSILFVGLIFGNSLIVIVFYMKLKYVASVFLNLALADCLFLLPLMAVITA 89
 QY 77 RRRHMAFGDIPCRVGLFTLANNRAGSIVFLVVAADRYFVHVPHNAVNTSTVRAAGIV 136
 DB 90 MEYRMPRGNTLCKIAGSVSEFNLYASVFLTCLSIDRYLAIVPMKS-RLRRTMLAKYT 148
 QY 137 C-TLMAVILITGVYLL-ENHLCVQETAVSCSFIMESANGMHDIMFOLE-----FMPL 189
 DB 149 CLIIWLAGLASLPTIIHRVFEIENTNITVCAFHYESQSTLPVGLTKNIIQGLPE 208
 QY 190 GILFCSPKIYVSLRRQOLARQARKKATRELINVAIV--FTCYLP-----SVSARLYF 243
 DB 209 -LIIITSYTLIMTKLKAWEIQNKRPKDDIFRIILAIVLEFFESVWPHQIFMDVILQ 267
 QY 244 LMTVPSSACDPVHGALHTLSTFTYNSMLDPLVYFSSPSPKRY----- 289
 DB 268 LGILRCKIEDIVDMPTTICLAFNNCLNPLFGFLGKRRKYFLDLKYIPKAKSH 327
 QY 290 ----NLIKISLKPQKQSHKTOPR 310
 DB 328 SNLSTKMSLTLSYRPSNGNSSTKRP 352
 RESULT 14
 ID 09G60 PRELIMINARY; PRT; 346 AA.
 AC 09G60;
 DT 01-DEC-2001 (Tremblrel, 19, Created)
 DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel, 20, Last annotation update)
 DE Unknown (Protein for IMAGE:3354783) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NCBI_Taxid=9606;

RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=EYE		
RA	Strausberg R.;		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases		
DR	EMBL; BC009522; AA009522.1; -		
DR	InterPro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm_1; 1.		
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.		
DR	PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.		
FT	1	1	
SQ	346 AA; 38790 MW; EA073A6CC05EBB72 CRC64;		

Query Match	16.3%;	Score 302.5;	DB 4;	Length 346;
Best Local Similarity	29.8%;	Pred. No. 1.3e-21;		
Matches 90;	Conservative 50;	Mismatches 135;	Indels 27;	Gaps 9;

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QY      13  TISQVMPPELLIVAVLALGNGVLAACECFEMHKTKWSPSTVLEFLAVADLMLCIPEPT  72
Db      18  TSNVLFIEFYVVCIIIGCGNTLVYIYLKRKKTKTNTIYIILNALADEFLMGDFELA  77

QY      73  DYLRRRHMAFGDIPCRVGLFTLLAMNRAGSIVFTVVAADRYEKRVPHHAIVTISTRVA  132
Db      78  -MQVALVHMPGKACICRYMIVDGINFTSIFCLTVASIDRYLAVVHPISAKWRPRRTA  136

QY      133  AGIVCTLMA--LVILG-TYVLLLENHLCQETAVSCSESFIMESANGMHD----IMPOLE  184
Db      137  KMIIMAVMGVSLVILLEIMYAGLRN--QMGRRSCTIMPGESGAMTGFIIITYFTILG  193

QY      185  FFMPLGIILFCSEKTVMSLR---RROQLARQAMKKATRFIMVAVIVFTTCYLPYSAR  240
Db      194  FLVEPLTTCICYFLIILIKVSSGIRGSSKRRKSEKKVTFMVSIVAVVFECWLP-----  248

QY      241  LYFLMTVPSASAC---DPSVGHALHLITSTYMNMSMDPLVYVEFSSPSFKFNKLKIS  296
Db      249  -FYIFNVSSVSMASIPSPALKGMDFVYVLTLYANSCANPLIYAFSLDNPFRKKSQNV-LCL  306

QY      297  LK 298
Db      307  VK 308

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RESULT	15
096TF2	
ID	096TF2
AC	PRELIMINARY;
DT	01-DEC-2001 (TREMblrel. 19, Created)
DT	01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT	01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE	Somatostatin receptor 2B.
GN	SSR2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20084417; Pubmed=10619399;
RA	Petersenn S., Rasch A.C., Fresch S., Bell F.U., Schulte H.M.,
RT	"Genomic structure and transcriptional regulation of the human
RL	Somatostatin receptor type 2."
EMBL	AF184174; AAF42810.1; -
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm.1; 1.
DR	PROSITE; PS00237; G_PROTEIN_REC_P.F1.1; UNKNOWN.1.
DR	PROSITE; PS50262; G_PROTEIN_REC_P.F1.2; 1.
SO	SEQUENCE 356 AA; 40006 MW; D10FA237FAED61F3 CRC64;

Query Match	16.3%;	Score 302.5;	DB 4;	Length 356;
Best Local Similarity	29.8%;	Pred. NO. 1.3e-21;		
Matches 90; Conservative	50;	Mismatches 135;	Indels 27;	Gaps 9;

QY	13	TISQVMPBLLIVAEVLGALGVGVALCGCFEMKTKWSPSTVYLFUVAADFLMLICPEFT	72
Db	41	TSNAVLFEIVFCVCIIGLCGNTLVIYILIRAKKTKITNTIYLALADELFHIGLPEFLA	100
QY	73	DYILRRRMAGSDIPCRKGLFTLLAMNRAGSIVPELTVAADRYEKVPHHAIVNTISTRVA	132
Db	101	-MOYALVHMPGKACIRVYMIVDGINOFTSIFCLTVASIDRYLAVVHAPISAKWRREPTA	159
QY	133	AGIVCTLMA--LVILG-TVYLLLENHLCVQETAVSCSEFIMESANCMHO----IMPOLE	184
Db	160	KMTMAVGVSLVILPIMIVAGLRSN--QWGRSSCTIMMPGSGMWYFGILLIYFTILG	216
QY	185	FEMPLGILLFESFETWSLR----RROQLARQAMKKAATFIMVVAIVFTCYLPSVSAR	240
Db	217	FLVPLTIIICLYEFLIIRKVVSSGIRGVSSKRKKSEKVTWVSIVAAVFLFCWMLP-----	271
QY	241	LYFLMTVPSSAC---DPSVGHALHILTSFTYMSMDPLVYVFSSPSPKPFNKLKGS	296
Db	272	-FYIFNVSSVSMALSPHPALKGMDFVYVLTLYANSCANPILLYNFLSDNFKKSPQNV-LCL	329
QY	297	LK 298	
Db	330	VK 331	

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Search completed: March 26, 2003, 19:38:47
Job time : 37 secs
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Job time : 37 secs

